DEVELOPMENT OF MODELS FOR THE GENETIC IMPROVEMENT OF DAIRY CATTLE UNDER COOPERATIVE DAIRYING CONDITIONS IN BANGLADESH

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This thesis is dedicated to my late parents

ABSTRACT

The aim of this thesis is to enquire into genetic approaches for improving milk yield from dairy cattle in order to overcome the milk shortage in Bangladesh. Survey work on the dairy industry was carried out to reveal its current status. The collected data of different genotypes (Pabna cattle, Australian-Friesian-Sahiwal × Pabna, Holstein × Pabna, Jersey × Pabna, and Sahiwal × Pabna) from 1999 to 2001, and in two seasons, were used to predict model parameters, fit-statistics and total lactation yields, by fitting ten lactation curve models. Best fitting model(s) were chosen on the basis of fit-statistics. The input parameters from best fiting model(s) were used for: developing a deterministic model; estimating the profitability of individual cows; estimating whole farm profitability; and for developing a profit function to estimate the economic values of traits in breeding objectives. The individual cow performances for different traits were stochastically simulated in respect of additive genetic, permanent and temporary error, herd and age effects, and mendelian sampling under progeny and parent-average testing breeding schemes based on three selection objectives applied over on 20 year period. Genetic gains in different traits were calculated from the regression of trait values on the selection index.

The estimated lactation curves model parameters, and predicted lactation milk yield were significantly different between breeds, years and seasons. From four fit-statistics values, the CCC value was considered superior, and this value indicated that the Nelder model best represented the test day records. The net annual income for Holstein × Pabna cattle was the highest (US$229) and was lowest (US$115) for Pabna cattle, while all other genotypes were intermediate. The economic values (EVs) of milk yield for all genotypes were similar (US$0.32), and due to payment for milk volume only, the EVs of fat and protein were negative. EVs of liveweight, calving intervals and calving rate were negative, but survivability was positive in all genotypes. The parent-average testing selection scheme showed higher genetic gains than progeny testing. The highest (US$15.80) genetic gain was obtained for milk yield when selection was for milk merit only.

The study will assist in undertaking a genetic improvement programme for the increase of milk production in Bangladesh and thereby enhance food security.

(**Key words**: Dairy cattle, genetic improvements, models, stochastic).

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CHAPTER ONE

General Introduction

Introduction

The total livestock population of Bangladesh comprises 24.4 million cattle, 34.4 million goats, 0.83 million buffalo and 1.14 million sheep (DLS, 2002). Approximately 46% of the rural households maintain dairy cattle, with the average number of cattle per household being 2.5 (Saadullah, 2000). However, in the cooperative dairying regions and for commercial farms, the herd size is larger and typically ranges from 5 to 100 cows, while occasionally reaching several 100.

The cattle of Bangladesh are mainly an indigenous Zebu type (*Bos indicus*) and their average milk production is 0.5 to 2.5 litres per day (Ahmed and Islam, 1987 and Hossain et al., 2002). Crosses of Holstein-Friesian, Jersey, Sahiwal and Red-Sindhi with indigenous cattle, produce 5 to 10 litres per day (Nahar et al., 1992; Majid et al., 1998 and Hossain et al., 2002). The country has two improved varieties of cattle, Red Chittagong and Pabna and they produce intermediate levels of 3 to 5 litres per day (Majid et al., 1998 and Khan et al., 2000).

Of the total domestic milk production in Bangladesh, the contribution by cattle is estimated to be about 64% (FAO, 2004) with the remainder being provided by goat and buffalo. Cattle, however, fulfil only 13.6% of the total milk requirement, and just 15.6% of the meat requirement of the country. Therefore, there is an acute shortage of animal products in Bangladesh and the demand is predicted to increase 2 to 3 fold by the year 2020 (BLRI, 2001).

The dairy sector of Bangladesh comprises a mixture of government, cooperative and family-oriented farms. The Bangladesh Milk Producers' Cooperative Union Limited (BMPCUL) is a large and well organized cooperative dairy industry, which is operating in 15 districts out of 64 in the country. The cooperative organisation plays a vital role in sustaining and improving the dairy industry, as in these areas, the cattle density is comparatively larger than in other parts of Bangladesh. According to Hemme et al. (2004), nearly half the milk production of Bangladesh comes from the Sirajong and Pabna districts, where the BMPCUL dairy plant is situated. An important reason for the expansion of dairying in this area, is that almost all the cattle in the area have an opportunity to graze on natural pastures, called Bathan, during the dry season (December to May). In addition, a well-developed marketing channel operates under BMPCUL. BMPCUL ensures regular collection of milk from cooperative members, and also provides necessary technical and logistic support for cow rearing.

The shortage of milk production in Bangladesh is mainly due to the low productivity of the cows. The cooperative farmers' main objective is to maximise the net farm income and profit. Since the low productivity of cows contributes to low profit, increasing milk production will improve the net income of BMPCUL members. Milk production could be improved by better feeding and/or management practices, as well as genetic improvement of the cows. Among these options, genetic improvement is a permanent and effective solution. For this to occur, genetic and economic evaluation of different breeds, and improvement of the genetic merit of individual cows is required.

One goal of dairy cattle breeding is to increase the genetic merit of cows for profitable milk production. Because profit is influenced by several traits, profit functions including these traits should be used. In tropical studies, Reddy and Basu (1985) and Madalena et al., (1990) used a profit function that, in addition to milk sales, included returns from sales of calves and culled cows. Madalena et al., (1990) concluded that maximum profit was obtained by utilizing F_1 heifers (Holstein-Friesian crossed with Guzera). Pure Holstein-Friesians showed higher profit than crossbreds (Gunjal et al., 1997; Kahi et al., 2000 and Khan et al., 2005). Within genotypes, profit functions can be used to estimate economic values (Kahi and Nitter, 2004 and St-Onge et al., 2002), which are required to define breeding objectives and to predict revenue from breeding programmes. Although there are some studies examining economic values for breeding programmes in tropical countries few have been undertaken in Bangladesh.

To obtain a single genetic value for the ranking of animals for selection, economic values are multiplied by the breeding value of the relevant traits, and the products summed across all traits affecting profitability to arrive at a single index value (Hazel, 1943). In recent years, the genetic evaluation of dairy cattle for lactation yields has been undertaken using test-day models (TDM) (Swalve, 1998; 2000; Jensen, 2001 and Powell and Norman, 2006).

Currently, there is no systematic genetic evaluation programme operating in Bangladesh to enable effective genetic improvement of dairy cattle. Ill-defined breeding objectives, inefficient artificial breeding programmes, small population sizes, improper recording, and a lack of infrastructure and skilled personnel are some of the major constraints for genetic improvement (Bhuiyan, 1997).

The main aim of this study is to propose an effective breeding scheme to improve the genetic merit of dairy cattle in the BMPCUL area of Bangladesh. To achieve this aim, the following steps were undertaken:

1. Dairy production systems in Bangladesh, including crossbreeding were reviewed (chapter 2 and chapter 3)

2. Production, processing and marketing systems of the BMPCUL area were surveyed (chapter 3).

3. Whole of lactation milk yields were predicted using various mathematical models to represent lactation curves (chapter 4).

4. A deterministic farm model, built on predicted milk yields, costs and income from individual cows was developed (chapter 5).

5. Economic values for traits in the breeding objectives and estimated genetic gains in the various traits were derived (chapter 6).

6. A multi-trait stochastic simulation model which predicted the genetic merit of individual dairy cattle in different breeding schemes was developed (chapter 7).

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CHAPTER TWO

Review of Literature

There is an acute shortage of milk and meat in Bangladesh and this leads to a poor nutritional status of the Bangladeshi people. Relieving the shortage of milk in Bangladesh requires efficient planning of the whole industry with consistent and objective breeding decisions aimed at the genetic improvement of dairy cattle. Several attempts have been undertaken for the genetic improvement of dairy cattle since 1970, albeit, due to constraints such as inadequate recording, small herd sizes and ill-defined breeding objectives, these programmes have not been entirely successful.

In Bangladesh, there are no well-defined recording systems and as a result the success of genetic evaluation of dairy cattle and research of different management schemes is challenged. For the understanding of farming systems the construction of simulation models can be helpful, enabling integration of knowledge of the components of a farm system together with their interactions. Such models assist researchers, policy makers and farmers in making decisions for the improvement of sustainability as well as farm profits.

For these research programmes, the total yield of an entire lactation is needed. Mathematical models of lactation equations assist in predicting the total amount of milk yield throughout the entire milking period, from the test day yield or incomplete lactation record. Moreover, it provides the shapes of lactation curves which indicate the milk production pattern.

The definition of the breeding objective should be the primary step in developing structured genetic improvement programmes (James, 1982; Harris et al., 1984 and Ponzoni, 1986). The breeding objective is defined as the combination of economically important traits of dairy cattle within the production system. It should account for inputs, such as food, husbandry and marketing costs, and for outputs, such as income from milk and beef sale. Decisions, about which traits should be included in the breeding objective, should be based on economic grounds and on whether they are difficult or easy to measure or change genetically.

This review is presented in five sections: mathematical models for the lactation curves; farm models within the dairy industry structure; the development of breeding objectives and the derivation of economic values; and multitrait simulation for index selection.

2.1 Mathematical models for lactation curves

2.1.1 Introduction

Milk yield is a primary trait in dairy cattle production. The positive correlation between test day milk yields and total lactation yield indicates the profitability of a dairy herd. Accurate description and predictions of lactation curves for cows are important, as they allow a better understanding of the production systems, and give useful information for the genetic improvement of dairy cattle. They are also relevant to conducting feeding trails with lactating cattle, estimating total lactation yields from incomplete records and forecasting herd performance on a monthly or individual cow basis (Sauvant, 1988). A mathematical model of the lactation curve provides summary information about dairy cattle production from the periodically recorded or incomplete data. This information is useful in making management and breeding decisions, and also in simulating the dairy enterprise. The patterns of lactation curves are also of interest for many practical purposes, e.g. health monitoring, individual feeding and also genetic evaluations. Therefore, the study of mathematical models for the lactation curve is important.

2.1.2 Lactation curves

The mathematical models of lactation curves are the functions of $y = f(t)$, which is defined by the positive value of daily milk production (y) and time from parturition (t), used in the dairy cattle industry for breeding and management purposes.

2.1.3 Types of lactation curves

Several mathematical functions have been proposed in the literature (Beever et al., 1991; Sherchand et al., 1995; Grossman and Koops, 2003), these functions are mainly linear and nonlinear type of models (Masselin et al., 1987). In linear models, parameters are linear functions of days in lactation, or some transformation of days in lactation, and can be easily computed by simple linear regression techniques.

Nonlinear models cannot be expressed as linear functions of parameters and, therefore, need iterative techniques to be solved (Masselin et al., 1987).

Models of lactation curves can be categorised into either empirical or mechanistic models. Empirical modelling presents milk yield (y) as a function of time (t). These models can be used to obtain information such as total lactation yield, peak yield, time of peak yield and measures of persistency of lactation after fitting the regularly recorded daily yield against the number of days in the milking period. Mechanistic models require hypotheses about the response of milk yield to various stimuli. Such hypotheses can be developed from both empirical studies of the lactation curve, and from physiological studies of lactation. The primary advantage of a mechanistic model is that by predicting the supply of nutrients to the mammary gland, the model can account for interactions between nutrients from the rumen, in so far as they are represented in the model.

2.1.4 Model selection on the basis of the shape of the curve and the fit statistics

Models are usually chosen on the basis of their ability to describe a specific pattern on the plane (t, y), characterised by an initial ascending phase to a peak followed by a steady decline, i.e. the standard form of the lactation curve. However, the models are also able to represent several other shapes. This is obvious for general functions such as polynomials, but it is also valid for equations specifically conceived to model the lactation curve (e.g., Wood and Wilmink functions) (Beever et al.1991). This feature is useful, for example, when considering other milk production traits (fat and protein content) or data relating to other species. Several shapes of lactation curves occur when milk test-day data are fitted with regression equations. Some consist of slight modifications of the standard curve, for example, the presence/absence of an inflection point in the decreasing part of lactation (Druet et al., 2003), whereas others are markedly different, as in the case of continuously decreasing curves that lack lactation peak (Congleton and Everett, 1980; Shanks et al., 1981 and Olori et al., 1999).

The number of parameters in a model and their degree of relationships are the main features of a typical lactation pattern, such as peak yield, time at peak and persistency. The analysis of relationships between mathematical properties of models, and lactation patterns has been focused mainly on the evaluation of fitting the performance. Curve modelling usually deals with data of homogeneous groups of animals, and almost all proposed functions are able to fit average patterns with a high level of accuracy. Individual patterns are also of interest when conducting research on feeding trials, estimating genetic merit, economic evaluation of different management schemes and when forecasting the herd performance for a specific period (Goodall, 1986 and Groenewald et al., 1995). In this case, due to the effects of several environmental and genetic factors that result in a random variation of shapes between cows, a large range of goodness of fit statistics such as: Akaike information criteria (AIC), Bayesian information criteria (BIC), mean square prediction error (MSPE), root mean square prediction error (RMSPE), R-square (R^2), Concordance correlation coefficients (CCC) have been reported by several authors (Wood, 1969; Pérochon et al., 1996; Olori et al., 1999 and Val-Arreola et al., 2004). On the basis of goodness of fit a set of suitable models for lactation curves may be selected.

2.1.5 Development of lactation curve

Mathematical models of lactation yields were developed in 1960 when Wood (1967) proposed the incomplete gamma functions:

$$Y = at^{b}e^{-ct}$$

where, Y is the average daily milk yield, in the t^{th} week of lactation, and a, b and c are parameters which determine the scale and shape of the curve.

This model takes in to account, the rise to peak lactation. Before Wood, other workers (Gaines, 1927 and Nelder 1966), proposed the prediction of lactation yields by using simple exponential decay models. However, they had limited accuracy, as they took no account of the rise to peak production of lactation. As Wood (1967) model provided the typical lactation curve shape, Wood then subsequently applied this model with the changes in liveweight, feed intake, milk cell counts, and yields of milk constituents during lactation, and this model became the standard model for application in many countries (Wood, 1979).

There were many attempts made after 1967 to improve the Wood model. These can be classified as; 1) improving the functional form of the model, 2) improvements in the mathematical properties of the model, and 3) attempts to produce forecasting models using a time series approach. Wood (1981) included a factor S_i to allow the seasonality of milk production or parity of the cows or region of the country, thus the model became:

$$Y = S_i a t^b e^{-ct}$$

Goodall (1986a) accounted for seasonality by use of a categorical variable D, which was set to 0 for winter production and 1 for summer production, the form of the model become:

$$\mathrm{Log}_e Y = \mathrm{Log}_e A + b\log_e n - cn + dD.$$

Papajcsik and Bodero (1988) listed 20 alternative functional forms for the lactation curve including the inverse polynomial model (Nelder, 1966), although some of the models listed, (such as the straight line) are unrealistic. Emmans et al. (1983) suggested that the cumulative yield of milk over lactation could be represented by a Gompertz function. Wilmink (1987) proposed a non-linear parametric curve with four parameters of the form:

$$Y = a + bt + ce^{-kt}$$

where, Y is the average daily milk yield, in the t^{th} week of lactation, and a, b, c and k are parameters which determine the scale and shape of the curve.

The parameters of this model can be reduced to a 3-parameter linear model by assuming the k exponent is of a suitable fixed value.

Rook et al, (1991) proposed a generalized form of the lactation curve,

$$Y = A\phi(t)\gamma(t)$$

where, A is a scalar, $\phi(t)$ is monotonically increasing with an asymptote at $\phi = 1$ and $0 \leq \phi(0) < 1$ and $\gamma(t)$ is monotonically decreasing with an asymptote at $\gamma = 0$ and $\gamma(0) = 1$.

The Wood curve fits this model except $\phi(t) = x^b$, which has an infinite asymptote. The model of Cobby and Le Du (1978) also has a similar form with $\phi(t) = 1 - e^{-qx}$ and $\gamma(t) = -kx$, and they found that using a linear function for the declining phase of lactation overcame the tendency of the Wood curve to underestimate in mid lactation and overestimate in late lactation in their data.

Cobby and Le Du (1978) attempted to improve the statistical properties of the Wood model by fitting non-linear square, or weighted log least squares, as opposed to the usual log least square approach. Dhanoa and Le Du (1982), Goodal and Sprevak (1984) and Goodal and Sprevak (1985) all proposed models which are similar to the Wood (1967) model.

Ali and Schaeffer (1987) proposed as a measure of estimation, polynomial regression, while Brotherstone et al., (2000) used the Legendre polynomial as a means of estimating lactation yields. In these models, random regressions and covariance functions have been used to compare the differences in model flexibility due to the number of parameters and the degree of correlation between them. Legendre polynomials of order 3, 4 and 5 were used to model the additive genetic and permanent environmental effects on the animal, and the same polynomials were included in the model as fixed regressions.

Jamrozik and Schaeffer (1997) modelled the lactation curve using a function of days in milk of the format:

$$Y = a_0 + a_1 t + a_2 t^2 + a_3 \ln t + a_4 \ln t^2$$

where, Int represents the natural logarithm of t,

Jamrozik and Schaeffer (1997) used the same covariate in their random regression model to describe fixed regressions and to model random deviations from the fixed curves. While these curves are non-linear to days in milk, i.e. the continuous scale along which records are taken, they are linear in the parameters of the curve (a_0, a_{1},.….a_4) and thus can be fitted in a linear model framework by regressing on the non-linear functions of t similar to regressing on Legendre polynomials of t.

The analysis of lactation records by empirical methods of curve fitting has been very common in dairy cattle. However, the parameters of some lactation curves derived by this method have little or no biological meaning, and moreover, provide little insight into what is happening to the animal during pregnancy and lactation. An early attempt at mechanistic modelling by Smith (1970), attempted to biochemically represent tissue metabolism in dairy cows. However, this work failed to simulate reality adequately, but it did identify adipose tissue metabolism as an important contributor to lactation. This work led to extended experimental investigations into adipose metabolism, and to an improved model for dairy cow metabolism being proposed by Baldwin et al., (1981). A well-formed mechanistic model of the lactation curve was described by Neal and Thornley (1983). They developed this model on the basis of functions of y = f (t). The model assumes the supply of metabolites being delivered by the blood, for milk synthesis and cell growth. Rook et al. (1993) and Dijkstra et al. (1997) proposed modified forms of mechanistic models, based on a set of differential equations representing cell proliferation, and cell death, in the mammary gland, which resulted in a 4-parameter equation.

Pollott (2000) developed a more complex mechanistic model which fitted logistic curves to represent secretery cell differentiation together with cell death throughout lactation. The resulting equation was:

$$Y = a\left[a/\left(1+\frac{1-b}{b}e^{-ct}\right)-1/\left(1+\frac{1-d}{d}e^{-gt}\right)\right]\left(1-e^{-ht}\right)$$

Where, parameters a, b, c, d, g and h define the scale and shape of the curve, t represents time for lactation.

2.1.6 Summary

- The models for lactation are of two general types: linear and non-linear regressions.
- Mathematical models of lactation curves are important for the genetic and economic evaluation of different management schemes.
- The models are able to represent the different shapes of lactation.
- Initially models for lactation curves were based on an incomplete gamma function but gradually developed into a more mechanistic type of model from the simple empirical model.
- Few studies have compared the different mechanistic models for their ability to accurately represent individual cow lactation curves.

2.2 Farm models

2.2.1 Models

According to Spedding (1988) as quoted by Doley (2002), models can be defined as "representations of the real thing, simplified for some purpose: they include those features that are essential for the purpose, and leave out those that are inessential" or more specifically as "an abstraction and simplification of the real world, specified so as to capture the principle interactions and behaviour of the system under study, and capable of experimental manipulations in order to project the consequences of changes in the determinants of the system's behaviour".

It is impossible to develop a model of an agricultural system representing of the entire system. Instead, it is necessary to develop a model emphasising those aspects required to meet the objective, or answer the question being asked. Models can relate to whole systems or to sub-systems. Where a system is complex, models of sub-systems can be developed and incorporated into the model as a whole, with outputs from a sub-model acting as inputs to another sub-model (Spedding, 1988).

2.2.2 Use and classification of models

According to Wilson and Morren (1990), the uses of the models are to:

1) communicate complex interrelationships;
2) communicate concepts about the meaning of something;
3) search for new insights about how a system is, might work or might behave; and
4) evaluate alternative strategies or changes.

Models can be used to identify when experimental studies are required to improve knowledge. Some models utilise and assess the results of such studies, and modellers are then in a position to form an objective and critical review of knowledge of the system (Dent and Blackie, 1979). A system approach can cope with complex hypotheses, or hypotheses on complex systems, often expressed only as computer models (Spedding, 1988).

The different types of models described by Dent and Blackie (1979), Spedding (1988), Dent (1990), Doyle (1990), Wilson and Morren (1990) and Sørensen (1998), are as follows:

1. Mental and verbal
2. Physical, also known as scale or iconic models. Standard symbols may be used to represent the various system components e.g. Forrester's symbolic language.
3. Diagrammatic models, including pictures and flow diagrams, which often use recognised symbols. This is often a preliminary phase to the development of a mathematical model.
4. Mathematical programming models, such as linear programming models. These models are typically optimisation models for decision support (Dent and Blackie, 1979; Sørensen, 1998).
5. Simulation models, which do not include optimisation algorithms, and are used to answer "what if?" questions (Sørensen, 1998).

The last three categories are known as symbolic models, of which 4 and 5 are mathematical models.

2.2.3 Simulation models

Simulation models were identified by Dent and Blackie (1979), Doyle (1990), Wilson and Morren (1990) and Sørensen (1998) as being useful when:

1. real-life experimentation is impossible or impractical because of time or cost factors, or the subject cannot be experimented on e.g. for economical, social innovation or ethical reasons;
2. real-life experimentation would disrupt the system to the extent that the results were artificial;
3. situations that do not exist are to be evaluated;
4. the effects of time are to be included in the analysis;
5. stochasticity is to be included in the analysis to evaluate risk; and
6. people are being trained to operate in a real-world situations.

Simulation models can be categorised according to type: Static or dynamic, deterministic or stochastic and empirical or mechanistic (Sørensen, 1998). Time is included as a variable in a dynamic model, whereas static models remain constant over time. Some variables in stochastic models use a single value described in terms of probability distribution, whereas deterministic models use a single value, such as a mean for all variables. The outputs from a deterministic model, given a set of inputs, will always be the same, whereas in a stochastic model the outputs will vary. A mechanistic model has one or more sub-levels whereas an empirical models relates to input within the same hierarchy. Jones and Luyten (1998) describe models as being continuous or discrete. Variables change smoothly over time in a continuous model (described by equations) whereas the variables in discrete models take on integer values (e.g. dead or alive).

2.2.4 Modelling process

In the modelling process, there are a number of variables or components involved.

> Exogenous variables are those outside the system boundary that affect the system (Dent and Blackie, 1979). These variables can be controllable or uncontrollable. Controllable variables can be fixed (represented by a constant), or can be systematically varied to assess their effect on the outcome. These inputs can also be known as driving variables, where they refer to a rate or ratio, or a source where they refer to a resource (Ebersohn, 1976 and Wilson and Morren, 1990).
>
> State variable are levels or amounts of materials, within the system.
>
> Rate variables refer to flows of action or materials within the system.
>
> Auxiliary variables are described as a mathematical function of other variables within the system. Outputs from the system to the environment, often the objective of the system, can be referred to as ‘sinks’. Components of the model that are considered to remain constant over time, are represented by parameters or constants (Jones and Luyten, 1998).

The steps involved (adapted from Dent and Blackie, 1979) for the construction of a simulation model are described below.

1. Define the systems and the modelling objectives: A model should have the outputs and inputs, the degree of detailed requirements, and the boundary as defined. Cooke (1998) notes that the decision-makers need to be identified and further suggests that the decision–makers are usually the person (and/or group) whose objectives are not being met as well as the resource provider. The statement of objectives should clearly define the intended users, and the end product required (Jones and Luyten, 1998). Furthermore, the available modelling resources (e.g. expertise, time, finances) and the environmental constraints (Ebersohn, 1976 and Cooke, 1998) should also be considered.

2. Data analysis: The information requirements of the model must be considered. A conceptual model should be developed as a first step in identifying which data are available, and that which needs to be generated. The objectives and conceptual models are stated in word form or sketches (Ebersohn, 1976 and Cooke, 1998).

3. Model construction: Firstly, it should be decided whether a simulation model is appropriate, or a simpler model would be sufficient. A diagrammatic model shows the components of the system, and their relationship to each other is then developed and a detailed data search is conducted to quantify the model components and relationships. The model construction process may be iterative requiring model restructuring. Data modification or manipulation may be necessary where data or functions to describe the relationships in the model are limited. Where data limitations mean a sub-system cannot be adequately represented within the system, a component can be represented as an exogenous variable instead. Alternatively, data can be purposely generated by experiments. However, this may be costly in terms of resources. A symbolic computer flow diagram may be developed with the final step being the development of the computer representation, using an appropriate programming language.

4. Validation of the model: Model validation ensures that the model mimics the 'real' system sufficiently accurately, to meet the models objectives (Spedding, 1988 and Jones and Luyten, 1998). The same inputs should result in the same outputs. Cooke (1998) suggested that an intermediate check can be performed to improve the accuracy of the model. The model should be tested against data not used in its construction (Dent and Blackie, 1979; Spedding, 1988 and Sørensen, 1998). However, this is not always possible. For example, a livestock system may require a fresh set of data from farms with the same production system measured over several years. In this case, model outputs should be sufficient to enable it to be compared with reality, and model validation is achieved through application (Sørensen, 1998). Further model modification and construction may be required. In reality, it is difficult to validate stochastic simulation models because the outputs will vary from the same inputs.

5. Sensitivity analysis: This can be part of the model validation, and/or model application sensitivity. Model parameters or variables that are sensitive and identified, are viewed, and the model outputs are scrutinised to ensure that they represent sensible volumes. If there are doubts about the accuracy of the model because of data limitations (modification of existing data or use of estimates), further modification of the model may be required. If the model is a good representation of the system then this identifies the areas where close monitoring or control may be needed in the 'real' system.

6. Model application: Documentation relating to model structure and computer code and comprehensive user documentation needs to be prepared (Jones and Luyten 1998). It should be sufficiently clear for users to understand the purpose of the model, and what the model can and cannot do.

2.2.5 Multitrait simulation models for selection index

The genetic simulation model was developed based on the principles and models of Middleton (1982), Tier (1984) and Falconer and Mackay (1997). The classical model of quantitative genetics is considered. The model is as follows:

$$P = G + E$$

Where, P = phenotypic performance

G = genotypic performance and

E = environmental performance

The environmental effects can be classified into (i) permanent, (those that affect performance throughout life) and (ii) temporary, (those that affect performance for a few weeks or months such as the level of feeding, stage of lactation and health status of the cows). The permanent and temporary environmental factors interact with the genotype of an animal, affecting feed intake and partitioning of feed, and consequently, the phenotypic expression of milk, fat and protein production (Oldham and Emmans, 1989).

Quantitative genetic models usually start with the simulation of genotypic values for a parent generation, followed by the transmission of those simulated effects to progeny, which then have a term added to simulate Mendelian sampling (e.g. Kennedy, 1986). The advantages of this type of simulation are:

(i) enables the effects of selection of breeding values and variance components to be examined (e.g. Sorensen and Kennedy, 1984a,b; Walter and Mao, 1985).
(ii) types of gene action including additives, maternal and epistatic genetic effects can be studied (e.g. Southwood et al., 1989).
(iii) the investigation of sampling variances for estimates of variance-covariance components for any data structure.

For multitrait simulation of selection indices in the dairy cattle industry, both deterministic and stochastic simulation modelling work has been undertaken by many workers (e.g. del-Bosque Gonzalez (1989) and Shepherd (1991). The effects of varying genetic merit on animal performance have been simulated by many workers (Congleton, 1984; Dijkhuizen, et al., 1986; Sørensen et al., 1992 and Sørensen et al., 2006). Under these models, genetic variation in animal performance was stochastic and animal nutrition was accounted for either empirically or deterministically. Genetic merit is represented by either breeding values (Congleton, 1984; Dijkhuizen et al., 1986; Lopez-Villalobos, 1998 and Sørensen et al., 1992). For example, in the simulation model by Congleton (1984), the milk production potential of a heifer was based on the pedigree index of the dam and sire, and the correlation (0.22) between the performance of the dam and daughter and Mendelian sampling.

A deterministic model was developed, examining a two tier open nucleus breeding scheme with the objective of evaluating the genetic gains on breeding value estimates (EBV) calculated using a BLUP animal model by Shepherd and Kinghorn (1993) and Kahi et al. (2004). They showed that the genetic gain and profit per cow for all schemes varied between breeding objectives. Furthermore, a stochastic simulation model for multiple traits within the dairy industry was developed by incorporating the biological parameters and management strategies at cow level for up to ten years with ten replicates (Sørensen et al., 1992) and for 25 years with 5 replicates (Sørensen et al., 2006). It was found that the effect of the culling rate upon milk production and liveweight gain per cow, depends on the feeding regime (Sørensen et al., 1992) and the rate of genetic gain (14 to 25 EURO per cow per year) varies with selection strategies (Sørensen et al., 2006).

2.2.6 Summary

- Agricultural systems are complex and multi-disciplinary, combining biological, physical, economic, management and social science components.
- A model is a representation of real-life, although being simplified in some aspects.
- The modelling process requires the definition of the systematic establishment of the objectives, analysis of the data relevant to the model, construction of the model, validation of the model, model application and the consideration of the relevance of model outputs.
- There are many approaches to developing a model, and the consideration of the objectives, before developing a model is required, to ensure the correct modeling approach is chosen.
- The simulation of quantitative genetic models start with the simulation of genotypic values for a parent generation, followed by the transmission of those simulated effects to progeny generation.
- For multitrait simulation in dairy cattle breeding, both deterministic and stochastic simulation have been widely used.

2.3 Dairy industry structures

A structured dairy industry exists when farming units are structured in such a way that a small number of animals (seed-stock or stud animals) are maintained in a nucleus where within breed selection is undertaken. A high proportion of animals within the industry are managed by farmers running commercial farms, such farmers purchase their animals/genetic material from the nucleus/seed-stock herds. Stud/nucleus breeders obtain a significant proportion of their income from the sale of breeding stock, whereas commercial farmers obtain their income from the sale of products (e.g. milk, meat etc.). Such a structure can be represented in a pyramid form consisting of tiers: nucleus, multiplier and commercial. Processors, retailers and consumers exist below these tiers (Harris et al., 1984; Blair and Garrick, 1994).

The importance of industry structure lies in its determination of the pattern of gene transmission through the population, and the potential rate of genetic progress as well as differences in genetic merit (genetic lag) between nucleus stock and commercial animals (Garrick, 1993). This also has a great impact on the cost effectiveness of the application of genetic and reproductive technologies (e.g. artificial insemination, embryo transfer, marker assisted selection and genomic selection).

An unstructured industry consists of a number of independent or closed herds, each having its own selection objective, and developing its own rate of genetic gain in the traits that each farmer/breeder considers important. Any new industry will typically go through this phase, where in each herd operates independently. The rate of genetic gain will vary from actual gains, made by farmers operating an effective selection programme, to zero gains for a farmer not imposing any selection pressure or, sometimes even genetic losses (Garrick, 1996).

Most dairy industries in developing countries fall into the unstructured category (Jasiorowski, 1991; Smith, 1988). This is one of the main reasons why little or no genetic progress is being made in these countries, and the application of new reproductive and genetic technologies (artificial insemination; and multiple ovulation and embryo transfer, MOET; marker assisted selection, MAS) have typically delivered little benefit. This is because developing countries did not and still do not have, adequate infrastructure for organising a large scale genetic improvement operation.

2.3.1 Closed nucleus breeding scheme

When replacement stock for the nucleus herd are bred entirely from within the nucleus, and the genes (sires) flow in one direction, from the nucleus into the commercial sector (Roden, 1994), this nucleus breeding system is defined as a ‘closed nucleus’ breeding system. In this system, the industry population is divided into two tiers: ‘nucleus’ and ‘commercial’. The nucleus is composed of a small population of genetically elite individuals, while the commercial sector forms the majority of the population. Sometimes there are three tiers; with the third intermediate tier being known as the multiplier. The primary function of multiplier is to multiply the genetic material of nucleus stock for sale into the commercial sector.

The closed nucleus structure is the most common structure in countries where dairy production is in the unstructured phase (Jasiorowski, 1991; Smith, 1988). Usually, a registration barrier exists between the nucleus and the commercial (two–tired) and also between the multiplier and commercial (three-tiered) tiers. This barrier is usually under the control of breed societies, and is primarily an attempt to maintain the genetic purity of the nucleus tier. Three tier breeding structures exist in some extensive livestock industries (Carrick and England, 1990). However, evaluations of optimal designs for three-tier schemes are scarce, due to the difficulties encountered in optimisation (James, 1989). Shepherd and Kinghorn (1992) described a methodology for overcoming these difficulties. The beef cattle industry in New Zealand is an example of a three-tier structure (Blair and Garrick, 1994).

There is a one-way flow of genes from the nucleus to the commercial tier, via the multiplier tier (if this exists). Therefore, genetic progress made at the commercial level is directed by improvements that occur within the nucleus. The differences in genetic potential, (genetic lag) between the commercial and the nucleus tiers is given by Garrick, (1993) as:

2 × generation interval in commercial tier × annual rate of genetic gain

For three-tiered structure, the commercial tier lags behind the multiplier tier by twice the commercial tier generation interval, and the multiplier tier lags behind the nucleus by twice the generation interval in the multiplier’s stock. However, in practice, this is not the case, as the multiplier breeders buy above average sires from the nucleus breeders’ and also apply selection of female replacements, which reduces the lag. The lag, usually expressed in years, is suggested to be about 10 years in the New Zealand beef cattle industry (Blair and Garrick, 1994). The two most important factors affecting the size of the genetic lag, are the age structure of the individuals in the lower tiers, and as well as the sources and merit of sires and dams used in the lower tiers (Nicolas, 1987).

2.3.2 Open nucleus breeding scheme

When replacement stock for the nucleus population is selected from both the nucleus and the base (commercial), leading to a two-way flow of genes, then the breeding system is becomes an 'open nucleus' breeding scheme. In this scheme, the animals are permitted to move in all directions between nucleus, multiplier and commercial units. Most often, it will be females that are moved between tiers, but sometimes sires are moved from the commercial tier to the nucleus or from the multiplier to the nucleus. However, it should be recognised that the movement of animals from the commercial tier into the nucleus may only take place if adequate recording has taken place in the commercial tier.

Reasons for the movement of animals from the commercial/multiplier tier, to the nucleus, were given by Garrick (1993) and Nicolas (1987) as:

1. Mendelian sampling can generate offspring in the commercial tier that may be superior to the average performance of their parents and it would be beneficial to include these animals in the nucleus.
2. When selecting for lowly heritable traits, the lower response per generation will reduce the size of the lag between nucleus and commercial females introduced into the nucleus.
3. If selection objectives change, favouring a trait that has either not undergone selection, or has been achieving little genetic change, then it is possible the commercial tier, having greater proportion of animals, will also have the majority of elite animals. It would be sensible to transfer superior animals from the commercial tier into the nucleus tier in order to increase the overall genetic merit.

There is some evidence that the annual rate of genetic gain following selection is increased, and that the rate of inbreeding is substantially reduced in an open nucleus breeding scheme, (James, 1977 and Sørensen et al, 2006). Sørensen et al., (2006) showed that in an open nucleus breeding scheme, the annual rate of genetic gain for milk production could be increased by 6.9% compared to a closed nucleus breeding scheme.

A popular form of open nucleus breeding scheme, is the ‘group breeding scheme’ or ‘cooperative breeding scheme’ (Jackson and Turner, 1972; Rae, 1974; Hight and Dalton, 1974 and Nicolas, 1987). In this system, a group of breeders and/or farmers come together and agree to co-operate in the formation and subsequent running of an open nucleus. They identify and transfer animals of high producing ability from the large commercial population into the nucleus, and in return transfer breeding stock from the nucleus to the commercial herds. Normally females are introduced from the commercial tier to the nucleus and sires are returned from the nucleus to the commercial. For a large population, the optimum nucleus size is 5 to 10% of the population size and approximately half of the female nucleus replacements should be selected from the base population, the rest being sourced from the nucleus itself (Jackson and Turner, 1972: James, 1977; Kasanta and Nitter, 1990 and Roden, 1994). This can be vary, and can be less than 1% in which case the nucleus should be closed after initial screening from the commercial population to establish the nucleus.

An open nucleus breeding system is superior to a closed nucleus system of the same size because of a higher expected mean genetic value of nucleus replacement, and because such a system integrates the farmer’s resources, reduces total costs and encourages more farmer participation (Bondoc and Smith, 1993).

For the dairy industry in most developing countries, genetic change is often made by purchasing germplasm from overseas. However, those concerned with the importation of genetic change have to be aware of genotype by environmental interaction. A genotype × environment interaction occurs when animals differ in their ability to perform in different environments (Falconer and Mackay, 1997). A number of studies have revealed this interaction within dairy cattle production (Boettcher et al., 2003; Kolver et al., 2002 and Veerkamp et al., 1994). This interaction may affect response to selection, because the ranking of a sires genotype in one environment may be different from their ranking in another (Dickerson, 1962; Butler-Hogg and Cruickshank, 1989; Bondec and Smith, 1993 and Annor, 1996).

2.3.3 Summary

- A dairy industry structure is defined mainly under two categories: structured and unstructured.
- Structured industry consists of tiers: nucleus, multiplier and commercial; this contributes to the transmission of genes through the population, and increases the potential rate of genetic progress. Most new industries will typically go through the unstructured industry where each herd operates independently resulting in with lower overall genetic progress.
- An open nucleus breeding scheme is superior to a closed nucleus breeding scheme of the same size, due to higher expected genetic progress.
- For the dairy industry in most developing countries, genetic change is often made by purchasing germplasm from overseas and caution should be excercised due to possible genotype by environmental interactions.

2.4 Development of breeding objectives for dairy cattle breeding and the derivation of economic values

The definition of the breeding objective should be the primary step in the development of a structured breeding programme (James, 1982; Harris et al., 1984 and Ponzoni, 1986). The breeding objective should closely align with the overall objective of the livestock business in which the animals are used, as they are the critical link, using genetically improved animals (Amer et al., 1998). However, care should be taken in defining the breeding objective. If it is poorly defined it may lead to economic deterioration of the population (James, 1982). The breeding objective is a statement of the economic worth of an animal from a genetic perspective (Harris et al., 1984 and Harris and Newman, 1994). The breeding objective can be defined as an equation based on economic values, and breeding values. It may be determined as a mathematical function, or sets of functions, which describe the contribution of various traits to production efficiency (Harris, et al., 1984). The breeding objective for the improvement of i traits is represented as:

$H = \Sigma a_i G_i$

Where H = breeding objective;

a_i = economic value for trait i; and

G_i = breeding value for trait i.

Dickerson (1962) stated that a breeding objective relevant to the increased efficiency of livestock is important to all consumers of animal products, as well as to livestock producers and thus to animal breeders and researchers. Decisions about which traits should be included in the breeding objective should be based on purely economical grounds and not upon whether they are difficult to measure (food intake), easy to measure (growth traits), difficult to change genetically (reproductive traits) or have been researched adequately (James, 1982). When net profit is chosen as the objective, all sources of income and expense should be taken into account. Theoretically this may be desirable, but practically it would be difficult to implement. Therefore, only the traits of major economic importance are typically included in the breeding objective.

The primary objective of all producers is to increase the net profit of their farming enterprises. Since the sire-breeder is providing replacement sires for the commercial farmer, their objectives should coincide. The objective should be defined in terms of performance and directed towards the increase of profit. However, the list of traits to improve can differ considerably between different sectors of an industry, namely breeders, producers, processors and consumers. Since it is the consumer's satisfaction that ultimately dictates produce price, preferences should be transferred back to the breeders through market forces, whilst making sure that the feedback messages from the consumer to the breeder is not distorted. In addition, the objective must relate to future requirements, since any genetic changes made by the breeder take considerable time to be passed on to the consumer. In some cases, the list of traits that the breeder wishes to improve will include characteristics expressed early in life (e.g. growth to weaning) as well as traits that are expressed late in life (e.g. longevity). The relative importance of various traits in the objective should account for the time of expression, as the rewards resulting earlier may be more valuable than those received later. This can be accounted for, by discounting, which differentially weighs returns for different periods of time (McClintock and Cunningham, 1974;

Cunningham and Ryan, 1975; Smith, 1978 and McArthur and Del Bosque Gonzalez, 1990).

The breeding objective should describe how well animals suit a particular production purpose, a given market and the environment. Breeding objectives will differ in different situations, but the basic principle will remain the same and that is the maximisation of profit.

Barwick et al. (1991) suggested that having a properly defined breeding objective offered several advantages:

(i) It helps breeders to use the combination of Estimated Breeding Values (EBVs) giving them optimum genetic progress in their particular situation.

(ii) It helps in planning of breeding for specific markets. The ability and capability to target specific markets successfully is, however, not an easy process (Thompson and Strickland, 1999).

(iii) It helps to use the EBVs more efficiently, and enhance the value of existing EBVs by relating their interpretation in terms of farm profit (Charteris et al., 1998).

(iv) It will provide financial reward throughout the whole industry.

Research on breeding objectives in temperate environments for the dairy industry has been widely discussed in the literature (e.g. McClintock and Cunningham, 1974; Dekkers, 1991; Visscher et al., 1994; Wolfová et al., 2005 and Veerkamp et al., 2002). However in tropical countries, including Bangladesh, research on breeding objectives for dairy cattle production has been limited.

Ponzoni and Newman (1989) suggested a set of steps to derive breeding objectives for domestic livestock, which will be discussed in the following sections.

2.4.1. Specifying the breeding, production and marketing system(s)

Specifying the breeding systems involves identifying the breed for which the breeding objectives will be defined, under a specific production system (Harris et al., 1984; Ponzoni and Newman, 1989; Barwick and Fuchs, 1992). This also specifies whether the animals will be purebred or crossbred. The role of the breed influences the proportion of genes present in various segments of the production system, such as nucleus and commercial herds and in different maternal or terminal sire lines.

In most tropical countries, the mating systems (purebreeding and crossbreeding) utilise the dual or multi-purpose nature of cattle, more especially in lesser developed countries, such as Bangladesh. In this situation, cattle are not kept solely for milk production, but are a vital source of meat, hide or skins, draught power, fuel and fertilisers for improving soil fertility. In a structured dairy industry, genetic improvement arises from the nucleus or seed-stock herd. The improved genotypes are then replicated in the multiplier herds that serve the commercial sector. This multi-level structure suggests that genetic improvement made in the seed-stock herds, must be directed towards use in the commercial sector, in order to satisfy consumer demands. In a conventional industry, improvement in the breeder's economic benefit is a major incentive for selection strategies to change (Howarth and Goddard, 1998). However, economic signals indicating consumer desire should migrate from consumers to seed-stock producers (MacNeil, et al., 1994).

The production and marketing system involves quantifying the number of animals, their feeding and management together with the marketing of their products. For example, Newman et al. (1992) described production and marketing systems by stating how many animals there were, how the animals were fed and managed, the age composition of the herd, and the replacement policy and ages of animals for culling and marketing. Defining herd composition helped identify the age and numerical distribution of the herd, the number of replacements required each year, the number of available animals in all classes, total milk, milk products and culled cows for marketing each year. All these are required for the calculation of economic values, as not all traits are expressed with the same frequency or at the same time. In addition, the nature of feed, labour, land, buildings and equipment requirements, and the corresponding costs of various stages, are all vital to accurately describe the system. The length of grazing periods, intensive feeding periods (supplementary feeding period) and feeding costs should be included in the production and marketing system. The management of animals and the replacement policy should also be specified.

There is a wide variety of production systems in tropical countries including in Bangladesh. They vary from fully intensive systems, where the land size is very small and animals are handled daily, to extensive pasture-based systems and other combinations, that is, the cattle graze during some periods of the year on pasture land but are fully intensive at other times. A detailed description of production and marketing systems has been made for livestock by Harris et al. (1984) which can be utilised in all species of livestock.

2.4.2 Identification of sources of income and expenditures

The identification of sources of income and expenditure in dairy cattle herds helps the development of a profit equation:

$$P = I - E$$

where profit (P) is a function of income (I) and expenditure (E) (Ponzoni and Newman, 1989).

Amer and Fox (1992) formulated a profit equation in the general form of:

$$\pi = f\,(XPCvCf)$$

Where X is a vector of traits or animal characteristics,
P is a vector of output prices,
Cv a vector of variable input prices and
Cf a vector of fixed input prices.

Cv and Cf are typically considered as constant for all levels of farm output.

Harris (1970) indicated that, in the development of a mathematical function to describe a livestock enterprise, I and E can be combined in different ways: either profit ($P = I - E$), return on investment ($\Phi = I/E$) or cost per unit production ($Q = E/I$). However, Ponzoni (1988) stated that when P was equal to zero, as suggested by Brascamp et al. (1985) and $\Phi = Q = 1.0$ the relative economic values from P, Φ and Q were the same.

The cost of animal products depends on the efficiency of three basic functions: reproduction, female production (milk) and growth of the young (Dickerson, 1970). To assess the economic importance of improvements within each biological component of performance, it is important to separate the total cost into (i) the producing and reproducing of female population as well as (ii) progeny growing to market size. Similarly, animal products are obtained directly from the female (milk) and from the growth of her progeny (meat). Therefore, revenue depends on the sale of milk, surplus heifers, and cull cows and bull calves, as well as the value per animal sold. Total costs depend on food intake, the value of food per kg, husbandry costs, health costs, marketing costs as well as fixed costs. Fixed costs are those costs incurred by the producer and independent of the level of herd production e.g. cow purchase costs. All other costs are variable may change with the level of production and also in time (Ponzoni, 1986).

2.4.3 Biological traits influencing revenue and costs

The profit equation is expressed as a function of biological traits impacting on revenue and costs, or both (Ponzoni and Newman, 1989). Choosing selection criteria and organising logically-based performance recording, is difficult unless traits needing improvement have been identified, and their relative economic importance has been established (Ponzoni, 1986). Ponzoni (1986) developed a simple profit equation, and economic values were derived by expressing this equation as a function of biological traits, including those corresponding to feed intake. All criteria having a major impact on efficiency of commercial production should be reflected in the traits chosen for the breeding objective (Fewson, 1993). It is clear that primary performance traits such as daily average milk yield, fat yield or protein yield have a major impact on profit margins. In addition to primary performance traits, there are also secondary traits such as fertility, longevity and calving interval, mothering ability, udder and body capacity and feed intake that must be considered for their impact on profitability. Morris (1980) pointed out that a large proportion (50-70%) of total herd food intake is required by breeding cows for non-productive (maintenance) purposes. Economic values for certain traits may be negligible; therefore, these traits can be excluded from the breeding objective (Weller, 1994).

2.4.4 Derivation of economic values

The economic value of a trait is defined as "the average change in farm profit per year, as a consequence of one unit of change in genetic merit of the trait considered". Economic theory suggests that optimising objectives at the farm level would result in adjustments in levels of variable inputs and outputs in response to a genetic trait change (Amer et al., 1994). The estimated effects of farm profits are commonly termed as economic values and are used in the selection indices to determine the weight to be placed on each breeding value, when selecting animals for profit. Therefore, the relative economic value for each trait is the amount by which net profit may be expected to change for each unit of improvement in that trait, holding all other traits constant (Hazel, 1943). Dickerson (1970) defined relative economic importance, in terms of expected reduction in cost per unit of equivalent output, rather than an increase in profit.

Economic values can be estimated by regressing the price of animals against breeding values available at the time of sale (Schroeder et al., 1992). However, multiple regression analysis could be complex if the breeding values of different traits are highly correlated, and it may be difficult to interpret the results (Amer, 1994). When using this method, an expected market trend for each trait should be considered, for deriving the economic values, because market price is never stable. This method considered only gross return without taking into account the cost of production. However, when deriving the economic value of a trait, the cost of production should be considered because the marginal return, from a small change to the current system is important. This method can be used in countries where no breeding value information is available. In these countries animals and animal products are usually traded, based on subjective assessments.

Economic values can be estimated using discounted expressions, such as: (i) discounted gene flow techniques (McClintock and Cunningham, 1974), or (ii) diffusion coefficients (McArthur and del Bosque Gonzalez, 1990). The diffusion coefficients method differs from the gene flow method in that it accounts for the delay between the birth of the animals and the first time expression for the improvement of the animals. The gene flow method accounts for the same delay between the joining and birth of the animal (Kluyts, et al., 2003). The number of discounted expressions is a function of the number of progeny or latter descendents of the animal in question, and the annual discount factors. The discount factors account for the economic benefits at time t being more valuable than at time t+1.

The details of the dairy farm model were described by Groen (1988). Deterministic and static dairy farm models were developed to study the extent to which economic values of production traits in dairy cattle breeding depend on production circumstances (Visscher et al., 1994). The outputs and inputs of the farm are calculated from the sale of milk and beef, and from feed costs, labour costs and other variable costs. Fixed costs include all the costs that are fixed (constant or discontinuously variable) in respect of the size of the farm.

Most studies in dairy cattle breeding schemes have assumed a single-trait breeding goal, i.e. milk production. A few simulations by Pedersen and Christensen (1989) which include more traits were all carried out using deterministic simulation approaches. The detailed methodologies are discussed by Brascamp et al. (1985); Smith et al. (1986); Groen (1989a); and Visscher et al. (1994).

Veerkamp et al. (2002); Visscher et al. (1994); Dekkers (1991); Petersen et al. (1985); Groen (1989b) and Beard (1988) estimated the economic values for several traits in dairy cattle (Table 2.1). The economic values for fat production was positive, and increased with the increases in fat output, in dry-matter intake capacity, and also the energy requirement per average lactating cow present (Groen, 1989b). In the basic situation, increasing carrier (water) and protein production also increases the ratio between energy requirement and dry-matter intake capacity. Increasing liveweight decreases this level, giving rise to lower energy density of the diet. The economic value of mature weight originates from an increased energy requirement for the replacement female stock, increased energy requirements for lactating cows, and the increased sale per kg of disposed young female stock and lactating cows. However, most of the studies, estimated positive economic values for fat yield in systems where the payment of milk was based on fat and protein (Bekman and Van Arendonk, 1993; Gibson, 1989; Groen, 1989b and Visscher et al., 1994).

In tropical studies, Kahi and Nitter (2004) derived the economic values from unit increases in genetic merit for various traits (values are shown in Table 2.2). The economic value for milk production was positive, but negative for fat yield. The negative value for fat was due to the energy requirement for producing more fat content where payment was for milk volume only. Among the reproductive traits, age at first calving (AFC), had a negative economic value, indicating that selection aimed at decreasing AFC would positively influence the overall profit. St-Onge et al. (2002) derived economic value using an empirical approach (Table 2.2).

They used data from two types of milk recording options: (i) the official option, in which milking data from each test-day were collected by authorized field supervisors, and (ii) owner sampler option, in which the producer was responsible for milk production recording. The economic values of fat production in the two testing programmes were similar. For conformation traits, there were highly positive economic values and negative values for capacity. Feet and legs were positive and comparatively higher in official herd than owner sampler herd. The mammary system received less emphasis lower in both sampler herds. Cows with better conformation, feet and legs and mammary system have a greater lifelong profit through a presumed longer herdlife.

The simulation models can be used to predict feed intake, and cow performance, on the basis of availability, and of quality of grass and other supplements and to also optimise insemination and culling policies. However, the use of such models can become difficult when there is insufficient knowledge of the production system under analysis (Groen et al., 1997). Models for income and expenditure of the traits of interest, assume that the current management practice is almost optimal, and uses observed data to maximise35the profit functions (Annor, 1996; Amer et al., 1996; Bekman and Van Arendonk, 1993; Newman et al., 1992; Ponzoni and Newman, 1989; Wilton and Goddard, 1996). These approaches were used in the present study of derivation of economic values under cooperative dairying in Bangladesh.

Table 2.1: Economic values for milk production traits obtained after per unit change of trait

Traits	Exchange currency								
	Dfl			IF£	AU$	Dfl	CA$	AU$	CA$
	Basic	Milk price (+20%)	Milk Price (-20%)						
Carrier	-0.13	-0.12	-0.13	-0.06	-0.02	-0.33	0.171	-0.03	0.70
Fat	7.97	8.05	7.91	0.68	1.09	1.04	6.46	0.87	
Protein	11.27	11.32	11.23	4.49	3.52	12.60	1.93	1.12	
Birth weight	7.35	7.26	7.42						
Mature weight	-0.92	-0.93	-0.92						
Survival				8.98	4.05				
Calving interval				-1.63	-0.58				0.30
Country	Netherlands[1]			Ireland[2]	Australia[3]	Netherlands[4]	Canada[5]	Australia[6]	Canada[7]

[1]Groen, 1989a; [2]Veerkamp et al., 2002; [3]Visscher et al., 1994; [4]Bekman and van Arendonk, 1993, [5]Gibson 1989, [6]Beard, 1988 and [7]Dekkers, 1991.

Dfl = Dutch Florin's; IF£ = Iris Pound; AU$ = Australian Dollar; CA$ = Canadian Dollar.

Table 2.2: Economic values for milk production traits obtained after a 1% increase in genetic merit

Traits	Exchange currency		
	Ksh	US$	
		Owner sampler herd	Official herd
Milk yield	18.93	1.92	2.42
Fat yield	-2.76	31.00	25.38
Age at first calving	-2.72		
Mature weight	7.90		
Survival	27.56		
Calving interval	2.65		
Productive life time	0.07		
Conformation		155.74	180.88
Capacity		-102.69	-29.29
Feet and legs		77.03	101.32
Mammary system		5.02	50.87
Country	Kenya[1]	USA[2]	

[1]Kahi and Nitter, 2004 and [2]St-Onge et al., 2002.

Harris and Freeman (1993) used a linear programming model to derive economic values for yield traits and herd life, under various economic conditions and production situations.The model allowed optimisation of the system over time, simultaneously optimised management resources and capital allocation as well as optimising the future genetic potential of the animal. A linear programming model can be written as:

$$\text{Max } z = c'x$$

Subject to meeting the following linear constraints

$$Ax\{\leq \geq =\}b$$

Where, z is the value of the objective function (e.g., net income), c is a $1 \times n$ vector of objective function coefficients per unit of activity (e.g. price per kg of milk yield) x is a $n \times 1$ vector of activity levels (e.g. amount of green grass fed) A is an $m \times n$ matrix of resource or technical coefficients (amounts of mega calories required per kg of fat yield) and b is a m × 1 vector of resource limits (e.g. total number of hours of labour available).

They reported two properties of linear programming. The first one is additive, in which levels of activities show additivity in their combined effect. The second one is proportionality, in which a multiplicative relationship exists between units of resource required, and the number of units produced. Solving a linear programming model involves making an organised plan for the activities. An optimal plan maximises the objective function and is feasible for satisfying the constraints (Sivarajasingam et al., 1984). Linear programmes are usually solved iteratively by using a simplex method of variant of this method (Harris and Freeman, 1993).

Harris and Freeman (1993) computed economic values for yield traits and herd life under various economic conditions, and production quotas. The economic values of milk carrier, fat and protein yields and herd life computed with no quota, milk carrier quota, fat quota and milk carrier and fat quota are shown in Table 2.3. The economic values for the yield traits have product limitations that are negative because the value of future genetic gains of yield traits under quota is the cost of production. The changes in economic values of herdlife reverses this trend, because as the revenue from milk and fat decreases, the herd (life) increases in value.

Table 2.3: Economic values of milk production traits obtained after quota, and in market conditions

Traits	Situations							
	No quota	Milk carrier quota	Fat quota	Milk carrier & Fat quota	Free market quota	Milk volume quota	Fat content	Milk volume & fat content
Carrier	36.13	-4.67	35.35	31.73	-0.08	-0.34	-0.08	-0.33
Fat	776.77	850.37	-39.27	722.09	5.70	5.44	-0.17	1.04
Protein	957.11	1319.14	1198.11	858.68	12.85	12.59	12.85	12.60
Herdlife	59.16	151.77	130.98	71.94				
Country	Iowa State[1]				Netherlands[2]			

[1]Harris and Freeman, 1993 and [2]Bekman and Van Arendonk, 1993.

Table 2.3 also gives the economic values of milk production traits at price levels of a free market situation, and under various quota systems (Bekman and Van Arendonk, 1993). Under a milk volume quota system, the economic values for milk (-0.34) was lower than in free market conditions. This difference is slightly greater than that found by Groen (1989b) due to different prices and production levels. As expected, the imposition of a fat quota turned the economic value for fat yield from positive to negative. In the case of multiple quotas, the economic values for milk and fat production were reduced, compared with a situation without quota, while the economic value for protein was relatively unaffected.

Selection index theory suggests that, the profitability, or total merit of animals, is a linear function of measurable traits (Hazel, 1943). However, sometimes, profits may be non-linear functions of the traits (Amer et al., 1994). Non-linear profit equations cause the economic value of a trait to change, according to the mean performance of the population (Goddard, 1983). A similar difficulty may arise when the economic value of a trait depends on management practices (e.g. herd size, age at maturity, cost of buildings etc.) employed by the farmer (Groen, 1989b). Pasternak and Weller (1993) developed an interactive computer procedure to calculate linear weights when profit functions were non-linear.

A bio-economic model considers population dynamics, and the nutrition, biological and economic performance of a whole herd. A bio-economic model for milk production systems was developed by Brockington et al. (1983) for small-scale milk production systems in South-East Brazil, by considering the population dynamics, nutrition, and the biological and economic performance of the whole herd. When bio-economic models are used, a large number of factors and complex production systems are considered simultaneously. Using such models, costs and revenues are obtained on the basis of real phenotypic performance, which depends not only on genetic potential performance, but also on feed resources, and feed intake capacity. Using bio-economic simulation models, the effects of genetic change on profit or production efficiency were examined, and economic values of traits in dairy cattle production systems were derived by Groen (1989b); Harris and Freeman (1993); Koenen et al. (2000); and Vargas et al. (2002). Economic values can vary between breeds, between sexes, or from country to country, depending on the varying production situations (Table 2.1) (Groen et al., 1997). Economic values may change while the breeding programme is in progress, if permanent shifts in the market demands occur, (Hazel, 1943). Groen (1989b) and St-Onge et al. (2002) showed that absolute and relative economic values vary, with fluctuations in prices and costs. Therefore, the calculation of economic values, requires adequate knowledge of the production system and may require modelling of the farming system (Wilton, 1979 and Elsen, 1988).

Models of farming systems can be used to derive economic values (Wolfova et al., 1995). Models can range from simple to complex sets of specialized equations with technical input/output relationships based on scientific knowledge. Modelling methods can be divided into simulation, dynamic programming and profit functions (Weigel et al., 1995). Harris and Freeman (1993) subdivided the simulation modelling into positive (data analysis) and normative (bio-economic modelling) methods. However, whatever method is used to estimate economic values, it is necessary to derive accurate profit functions (Von Rohr et al., 1999).

The estimation of economic values depends on the prediction of future production system characteristics, including future prices. It is good to revise economic values within reasonable intervals of time.

2.4.5 Selection criteria

The selection criteria are the characters measured to predict breeding values of the traits in the selection objectives. Ponzoni and Newman (1989) stated that a clear distinction should be made between the traits in the breeding objective and characters used as selection criteria. According to the Barlow (1987), the factors to be considered for choosing traits as selection criteria are:

- (i) Is the character heritable?
- (ii) Does the character correlate to traits in the breeding objective and
- (iii) Can the character be measured simply and cheaply?

Sometimes, the set of selection criteria used in a selection programme can be the same as the set of traits included in the breeding objective. For example, Ponzoni and

Newman (1989) included calving days in the objectives, and also used this trait as a selection criterion.

The selection criteria should be adjusted for measurable environmental variation, such as the age of the dam, herd and sex effects. This assists in making selection more accurate (Harris et al., 1984) and to improve the rate of genetic gain (Blair, 1989).

The traits used as selection criteria should be weighted properly and included in a selection index (I) (section 2.4.7).

2.4.6 Phenotypic and genetic parameters

To derive weighting factors for characteristics in the selection index, heritabilities, genetic and phenotypic correlations among criteria and traits within the objective and phenotypic variation among the parameters, are needed. Detailed definitions, characteristics and methods of estimating these parameters have been described by several authors (Hohenboken, 1985; Nicolas, 1987 and Falconer and Mackay, 1997).

Blair (1989) stated that genetic correlation should be accounted for in any selection programme because:

(1) If two characters are related, the consequences of increasing one upon the response of the other, can be assessed e.g. an increase in milk yield can result to a decrease in fat percentage, due to the negative correlation of this two traits.

(2) The accuracy of selection, by using information on all related traits, in estimating the breeding value for any one trait, is enhanced.

(3) If characters are related, there may be an opportunity to select one character, thus bringing about a related or correlated response in a second character, which might prove more costly to measure.

The theory of the genetic selection index as developed by Hazel (1943) and later by Henderson (1963) among others, is based on the assumption that the population parameters are known with precision. To predict response to selection, the estimation of these parameters is necessary and should come from experiments with the specific breed used in the breeding system, and should also involve all the traits in that selection programme.

The expected response in the aggregate genotype (H) from selection based on a selection index (I) can be affected by sampling errors in the estimation of genetic parameters used in constructing an index (Hazel et al., 1994). The reasons why estimates of parameters can be inaccurate are as stated by Hill (1981):

(i) they may be come from another population, and therefore were not appropriate,

(ii) they may be from a different generation, e.g. the base population rather than current population after some generations of selection, or from the current population which is under selection, can be obtained from relatives of selected individuals and be biased, and

(iii) all estimates are subject to sampling errors, due to the limited number of animals that can be recorded.

The errors tend to increase as more traits are included in H, although, accuracy of estimation can be increased by using large data sets.

2.4.7 Methods of selection

The aim of animal improvement through breeding is to choose animals which have the greatest combined genetic value, to become parents for the following generation. The value of the animal is usually affected by several traits. Therefore the breeder has to be considered all traits when choosing the most suitable animals to parent the next generation. There are four methods for selecting animals for multiple traits: tandem selection, independent culling levels, selection of extremes and selection index. Among the selection methods the selection index method are more effective to ceate the genetic changes and this methods will used in this thesis, therefore the selection index method only will be discussed.

The selection index combines the available phenotypic information into a single score reflecting the merits and demerits of all traits. Hazel (1943) first applied the selection index theory to animal breeding. Since then, many workers have studied the selection index theory, including reviews by Legates and Lush (1954); Henderson (1963); Vandepitte and Hazel (1977); Philipson et al. (1994) and Hazel et al. (1994).

The definition of a selection index is a weighted linear function of selection criterion or breeding values, for each trait in the objective, with weights reflecting their relative importance. The equation for selection index is:

$I = \Sigma b_i X_i$ (i = 1, ……..n)

where I is the aggregate selection index which predicts the true genetic value of animals;

b's are the weighting factors of the selection criteria;

X's are the adjusted phenotypes of the selection criteria.

The elements of b are chosen to maximise genetic gain in a goal (aggregate) breeding value or breeding objective, are defined as:

$H_T = v'a$,

where v is an $m \times 1$ vector of economic values (weights); and

a is an $m \times 1$ vector of breeding values for the traits in the breeding objective.

The optimum selection index weights maximise the correlation (r_{HI}) or minimise the squared deviation, between the selection index and the aggregate genotype (breeding objective) and minimise the prediction error variance (PEV) (Weller, 1994). Hazel (1943) showed that maximum r_{HI} is achieved when $P_b = G_v$.

Selection index weights are then calculated as:

$b = P^{-1} Gv$,

where G is an $n \times m$ genetic variance-covariance matrix for m traits affecting

profitability and n correlated indicator traits incorporates the additive genetic relationships between sources of information;

P is an $n \times n$ phenotypic (co)variance matrix of correlated indicator traits;

and v is an $n \times 1$ vector of relative economic values.

Henderson suggested an alternative method of calculating index values (Hazel et al., 1994). The first step being the estimation of individual breeding values for each trait, through multitrait analysis, and the second being the application of relative economic values such that:

$$H = \Sigma a_i G_i.$$

The advantage of this separation is the permitted use of Best Linear Unbiased Prediction (BLUP) techniques in estimating the individual breeding values for each trait including adjustments for differences in information. Economic values can be varied according to differing selection objectives, depending on how different breeds are used in a breeding system, or the particular production and marketing system, without requiring the recalculation of the breeding values.

Generally, it is not feasible for individual breeders to develop their own selection index due to the complexity involved in deriving relative economic values for component traits, and accurate estimates of heritability, variability, and genetic and phenotypic correlations (Hazel et al., 1994). For this reason it is helpful for an animal breeding enterprise to become part of a larger organisation that facilitates data recording, and can compute individual breeding values of economically important traits, while using information on relatives using genetic parameters appropriate for the production system. The breeder can then apply the economic values considered to be most appropriate for the breed role and for the production and marketing system to be served, to obtain individual animal selection indices. This point suggests that it is very important for developing countries to organise the structure of their industries, while defining their breeding objectives.

2.4.8 Summary

- Effective animal breeding relies on detailed knowledge of the system involved, as well as the development of sound breeding objectives.
- Knowledge of the environment where animals will be found, along with the markets where products will be sold, must be known in order to formulate an effective breeding programme.
- Performance recording is important in assisting with breeding and management programmes, and also to improve informed decision making.

- Estimation of necessary parameters such as economic values, heritabilities and genetic and phenotypic correlations are the backbone of an effective breeding operation.

2.4.9. Genetic gains

The expected response to selection or rate of genetic gain within one generation can be predicted by calculating the average BVs of the individuals' chosen as parents. However, breeders are often interested in predicting response over a longer time frame than one generation. The change in the genetic merit from one generation to the next is:

Response per generation = (standardized selection differential × accuracy of selection

× genetic standard deviation)

or Response per generation = $\bar{i}\, r_{TI} \sigma_T$

where, $\bar{i}$ = selection intensity,

r_{TI} = accuracy of selection and

σ_T = genetic standard deviation.

In dairy cattle breeding, one sire can be used to inseminate more than 100,000 cows in a year, so sire selection typically has a greater impact on genetic gain, than female selection. However, it should be remembered that both sexes of parents contribute half their genes to the offspring.

Responses per year can be calculated by dividing response per generation, by generation interval. Thus,

$$\Delta G = \text{(response per generation)/(generation interval)}$$

$$\text{Or, } \Delta G = \frac{\bar{i}\, r_{TI} \sigma_T}{L}$$

The young bulls and heifers are taken in the breeding herd on the basis of their parent's performance in order to be chosen as a potential parent for next generation. The decision as to which of these animals actually will pass their genes on is made on the basis of some measurement of their own genotype - by own performance in cows and by progeny tests in bulls. Genes are transmitted to the next generation in four ways, which are: bulls to breed bulls, bulls to breed cows, cows to breed bulls and cows to breed cows.

By using the three determinants of superiority of selected animals, that is intensity of selection ($\bar{i}$), accuracy of selection ($r^2=\sqrt{R}$) and standard deviation of genetic values (σ_g) with four pathways or opportunities for selection results in Rendel and Robertson (1950) the annual rate of genetic gain (ΔG) in dairy industry can be calculated as:

$$\Delta G = \frac{\left[\bar{i}_{BB}\, r_{BB} + \bar{i}_{BC}\, r_{BC} + \bar{i}_{CB}\, r_{CB} + \bar{i}_{CC}\, r_{CC}\right]\sigma_g}{L_{BB} + L_{BC} + L_{CB} + L_{CC}}$$

Where, subscripts BB, BC, CB and CC refers to the bulls to breed bulls, bulls to breed cows, cows to breed bulls and cows to breed cows pathways respectively; the term in the denominator (eg L_{BB}) refer to the lengths of generation interval; $\bar{i}$ denotes to the intensity of selection and r is the measures of the accuracy of selection in respective pathways (Note $r^2=\sqrt{R}$ where R is the reliability of an estimated breeding value or breeding worth) and σ_g is the genetic standard deviation of the selection objectives.

Several authors (e.g. Smith, 1962 and Powell, 1977) have been used different method for the estimation of genetic gain for the economically important traits of dairy cattle. Smith (1962) estimated the genetic gains based on the regression of daughter performance on time. Burnside and Legates (1967) developed a method to adjust first-lactation records of first-born fuI1 sisters for favorable environmental effects that bias estimates of genetic gain from Smith (1962) equations. Schaeffer et al. (1975) and Powell et al. (1977) have been estimated genetic gain by regressions of sire’s average genetic merit on time. However, in all methods the rate of genetic gain could be improved by increase the accuracy and/or by reproductive developments that allow more offspring per sire (eg AI), more offspring per dam (eg MOET), or a reduction of the average age of the parents.

The factors that affect the rate of genetic gain:

1. Intensity of selection - determined by the proportion of available animals selected as replacements. This depends upon the number selected, also availability.

2. a factor derived from regression of true on estimated genetic merit. This factor usually includes heritability, but may be more complicated than shown the simplest case of direct selection.

3. The genetic standard deviation - a measure of the extent of genetic differences amongst animals in the population. This term really measures the amount of raw material currently available in the population. This factor is the most difficult to manipulate, other than by increasing genetic variation from the immigration of new genes.

4. The generation interval - a measure of how quickly progeny will be allowed to replace their parents.

It is tempting to use the above list to come up with a set of rules for increasing the rate of genetic gain. For example, response will be increased by:

a) increasing selection intensity. This is achieved by reducing the proportion selected, through making more animals available for selection, or through using fewer parents (especially males).

b) reducing the generation interval. This turns over the generations faster and can be achieved by using animals as parents at an earlier age, and by culling parents before becoming too old.

c) Increasing reliability of estimated genetic merit. This can be achieved by collecting more phenotypic information on an animal or its relatives, for example by progeny testing.

However,
These factors (a), (b) and (c) interact, the resulting in a net effect of changes when interactions are involved. For example:

- Culling at a younger age will reduce generation interval. However, it will also increase the number of replacements required to maintain population size. The need for more replacements will increase the proportion selected and reduce the intensity of selection.
- Using animals initially at a younger age, e.g. yearling bulls and heifers.This will reduce generation interval, but may also decrease the reliability of selection. Selection on fleece traits usually requires waiting until after hogget shearing, beyond the time at which mating has normally occurred.
- Progeny testing animals to increase reliability of ranking will usually increase the generation interval.

Rendel and Robertson (1950) showed that the contribution of the four paths of genetic progress to total genetic progress were:

$$\Delta G = \frac{(\Delta SS + \Delta DS + \Delta SD + \Delta DD)}{(I_{SS} + I_{DS} + I_{SD} + I_{DD})}$$

Where, SS = Sires of sires
DS = Dams of sires
SD = Sires of dams and
DD = Dams of dams

Sires of sires are used by AI organisations to produce young sires for sampling. The SS contribute most to genetic progress, as they are few and highly selected. In addition to intensity of selection being high for SS, the accuracy of selection is also high because all SS are progeny tested and r_{TI} ranges from 0.7 to 1.0.

Dams of sires are highly selected from out of the 2% of all cows in the population. Accuracy of selection is less than the SS path, ranging from 0.5 to 0.65.

Sires of dams are already chosen but farmers have limited option to select the sires to breed their cows. Intensity of selection is high but less than for SS.

The rate of genetic gain is dependent on the number of young bull tested with the cow population. For example, Robertson and Rendel (1950) showed maximum rate of improvement of 1.69% per year compared with 1% per year in a closed herd without progeny testing when 40 bulls mated with 1200 cows. Optimum number of progeny per tested bull maxmises the genetic gain per generation (Oliveir and Lôbo, 1995), they showed greater genetic gain can be achieved when 13 of total 550 available males are selected to be progeny tested with about 38 progenies per young sire.

Dams of dams are chosen by dairy farmers to leave female offspring in the population. The DD path contributes the least to genetic progress because the need of replacement females, results in a low selection pressure.

The actual progress is less than half the theoretical progress in dairy cows for milk production (Everett, 1983; Everett et al., 1976, Hintz et al., 1978 and Robertson and Rendel, 1950). The annual genetic progress in the registered Holstein female population was less than 1% of the mean (Lee et al., 1985). Maximum genetic gain was estimated at least 2% per year for artificial insemination populations of at least 10,000 cows (Specht and McGilliard, 1960). The theoretical limits are compromised in every path by decreases in the accuracy and intensity of selection. Accuracy is decreased by preferential treatment, and the use of non-AI sires. Intensity of selection is reduced by emphasis on secondary traits. Van Vleck (1977) reviewed potential causes for differences between theoretical and actual progress. However, gains in selection experiments exceeding theoretical expectations have other causes. A consensus from

several reports (Lofgren et al., 1985; Meland et al., 1982; Pearson et al., 1981; Powell et al., 1980 and 1983) indicates interaction of response to sire selection with herd means and variances. Also heritabilities increased with an average yield of herd (Pearson et al., 1981 and Powell and Norman, 1984). Interactions of genotype by environment are emerging as important for planning breeding strategies in developing countries, especially tropical areas (Abubakar et al., 1984, McDowell, 1983 and 1985) and in poor environments in Asia and Africa, the ¾ Holstein crossbreds were equal or exceeded slightly F_1 crosses in milk yield. However, they had a higher mortality rates, lower reproductive performance and shorter herdlife (Katapatal, 1979 and Kiwuwa et al., 1983, McDowell, 1983 and 1985 and Trail and Gregory, 1981).

In practice, every situation needs to be addressed individually using appropriate equations to predict the rate of genetic gain. Factors such as reproduction (age at puberty, reproductive capability) and measurements (time of recording relative to mating, sex limitating traits, eg milk yields) would impact the effectiveness of alternative strategies for a selection programme.

2.4.10 Summary

- genetic gains provide knowledge that show the selection programme as effective.
- genetic gain is optimised by balancing increasing selection intensity, reliability and generation interval.
- actual progress is less than half the theoretical progress of dairy cows for milk production.

2.4.11. Conclusion

This review described: a) mathematical models for lactation curves: it revealed that these are important for the calculation of total lactation yield, from test day yield, or incomplete data which helps for genetic and economic evaluations of different management schemes for dairy cattle breeds. It can also be seen that, more mechanistic models were gradually developed from a simple empirical model, based on an incomplete gamma function; b) farm models in the dairy industry structure: agricultural systems which are complex and multi-disciplinary, combining biological, or physical, economic, management and social science components. A model is a representation of real life, and modelling processes require definition of the system of establishment of objectives, analysis of data relevant to the model, construction of the model, validation of the model, model application and the consideration of the relevance of model outputs. Simulation of quantitative genetic models involve starting with the simulation of genotypic values for a parent generation, followed by the transmission of those simulated effects to the progeny generation. For multitrait simulation in dairy cattle breeding, both deterministic and stochastic simulation have been used; c) The development of breeding objectives and derivation of economic values: an effective animal breeding programme depends on detailed knowledge of the system involved, and the development of sound breeding objectives, within the environment and market situations. The estimation of parameters such as economic values, heritabilities and genetic and phenotypic correlations are important for an effective breeding operation; and d) Multitrait simulation for index selection: index selection is the most effective method among various selection methods.

Dairy cattle breeding and management involves decisions followed by actions. Decisions are based on information of the environment, market, and traits and on differences between animals and groups of animals. The better the information, the better the decisions, the more effective the actions, the better the chances of increasing profitability.

Performance recording is the systematic measurement of performance traits, or indicators of performance. These records become a data bank, which with correct manipulation and analysis, are used in breeding and management programmes that enhance decision making. Performance recording will increasingly be involved in maximising the value of information per unit of investment, in terms of either money and/or time. However, there is no well-developed recording system currently for genetic evaluation of dairy cattle in Bangladesh.

Hossain et al., (2002) and Hirooka and Bhuiyan (1995) estimated additive genetic and heterosis effects on dairy performance. They showed the additive breed effects on both the total lactation period, and daily milk yield were positive, and highly significant between *Bos taurus* and *Bos indicus*, whereas the individual heterosis effects were not. The effect of Friesian incorporation in local cattle was reduced, when grading up with the Friesian was repeated more than twice (Hossain et al., 2002). Hirooka and Bhuiyan (1995) reported negative and non significant heterosis effects on daily milk yield in crossbred of Bangladeshi local and Holstein. Similar results were reported by Taneja and Bhat (1974), who found a small and non-significant heterosis effect on milk yield of Sahiwal and Friesian crossbreds, whereas Sharma and Pirchner (1991) showed positive heterosis when crossing Friesian with Sahiwal breeds. The high levels of heterosis effects in both individual and maternal traits in crossbreds of European and indigenous Zebu cattle were reported by Cartwright et al., (1964); Koger et al., (1975) and Madsen and Vinther (1975). There are some studies on genetic parameters estimation of dairy cattle production (Hossain et al., 2002, and Islam et al., 2004). Although, these studies did not address the selection experiments for dairy cattle improvement.

The major constraints for genetic improvement of dairy cattle in Bangladesh are: ill-defined breeding objectives, inefficient artificial breeding programmes, small population size, lack of infrastructure and a shortage of skilled personnel. An increase in milk production in Bangladesh may be achieved through improvement of the nutritional status, and the genetic potential of the available dairy cattle. In Bangladesh, research on genetic parameters, estimating genetic merit of available genotypes, economic evaluation of different breeds in different management schemes, and the genetic improvements programmes of dairy cattle, is limited.

The Bangladesh Milk Producers Cooperative Union Limited (BMPCUL) is a well-organised large cooperative dairy production system. Under this dairy production system, it is possible to organise a dairy cattle genetic improvement programme sometime in the near future. Therefore, reviews, a survey study on productive, reproductive and marketing systems of dairy cattle production under BMPCUL areas; models on the lactation curves of different breeds in order to predict the total lactation yield from incomplete lactation records, development of a dairy farm model for economic evaluations of different genotypes, development of a breeding objective, and development of a multitrait simulation model for total merit of dairy cattle, are undertaken in subsequent chapters.

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CHAPTER THREE

Review of Bangladesh Dairy Production Systems, including Crossbreeding and a Study of the Production, Processing and Marketing of Cooperative Dairying in Bangladesh

3.1 Basic concept of Bangladesh

3.1.1 Geography and climate of Bangladesh

Bangladesh is situated in the north-eastern part of South Asia (Figure 3.1), between 20°34′ and 26°36′ north latitude and 88°1′ and 92°41′ east longitude, and is located between India and Myanmar. The southern frontier of Bangladesh is guarded by the Bay of Bengal, a deltaic region of the rivers Ganges, Brahmaputra and Megna. The country is mostly flat, except for ranges of hills in the northern and southeast regions. The total area of Bangladesh is about 143,998 square kilometres with a human population of 141 million (BBS, 2007) and population growth rate of 1.54%. The population density per square kilometres is about 954 (BBS, 2007). The topography of Bangladesh can be divided into four main ecological zones; rainfall or flood-fed land, wet-land, hilly and coastal.

Figure 3.1: Map of Bangladesh. Source: http://www/maps-of-the world.com/map pages/Bangladesh_map.htm search on 14 may 2008).

The climate is tropical, with a mild winter (November-February), hot humid summer (March-June) and humid warm monsoon (July-October). The average maximum temperature is 35°C and the average minimum temperature is about 8°C. The annual rainfall ranges from 1500mm to 6800mm (Bangladesh Meteorological Department, 2005).

3.1.2 Contribution of the agriculture and livestock sub-sector, to the economy of Bangladesh

The agricultural sector of Bangladesh accounts for about 19.7% of the national Gross Domestic Product (GDP) (BBS, 2007). The livestock sector contribution to GDP has increased from about 7% to 10% from 1997 to 2007 (BBS, 2007).

3.1.3 Land use in Bangladesh

There are about 12.33 million hectares of land used for cultivation throughout the year. Within farming households 58% are small farmers (less than 0.61 hectares), 12% are classified as medium-sized farmers (0.61 to 3.04 hectares) and 2% are large farmers (more than 3.04 hectares). Out of the total households, 28% have no cultivatable land at all (BBS, 2002).

3.1.4 Dairy farming in Bangladesh

Dairying in Bangladesh is mostly integrated with crop farming with 1-2 cows and 0.20 hectares of land per farmer being typical. In addition, there are some medium and large commercial farms (5-100 cows) around larger cities such as Dhaka, Chittagong, Rangpur, Khulna and Sylhet, that farm mostly Holstein-Friesian (H) and H crossbred cows producing milk for the farmer’s family consumption, and with any surplus milk being sold.

There are nine governmental farms, six under the control of the Ministry of Fisheries and Livestock (MOFL) and three under the control of the Ministry of Defence (MOD). The main objective of the MOFL is to produce high-yielding heifers for farmers. In addition, there is a large cooperative dairy production system, the Bangladesh Milk Producer’s Cooperative Union Limited (BMPCUL). The members of the cooperative milk mainly Pabna cattle and its crossbreds.

There are also two other institutional farms, one of which is under Bangladesh Livestock Research Institute (BLRI) control, and another under the Bangladesh Agricultural University (BAU) control. These herds maintain approximately 6000 cattle of different genotypes such as, Red Chittagong, Pabna, Sahiwal, Red-Sindhi, Holstein, Jersey, Holstein-Friesian crosses, Jersey crosses and Sahiwal crosses (Faruque and Bhuiyan, 2002).

3.1.5 Increased cattle/buffalo numbers and reasons

Between 2000 and 2005 the number of cows in Bangladesh increased by about 1 percent, while the buffalo population increased by about 4 percent (DLS, 2002). This increase in the number of cattle was due to the success of artificial insemination, and also the importation of animals from India. The main reasons for the increase in buffaloes were the establishment of the Rampal Artificial Insemination Centre in Bagarhat District and a loan programme for buffalo rearing.

The following sections review production, processing and marketing in the Bangladesh dairy industry, with an emphasis on cooperative dairy production.

3.2 Dairy production, processing and marketing systems in Bangladesh

3.2.1 Breeding and improvement

Bangladesh has a long history of dairy cattle breeding. For the improvement of indigenous zebu cattle, the tropical breeds Red Sindhi, Sahiwal and Hariana, were introduced in 1937, and the temperate breeds, Holstein-Friesian and Jersey, were introduced in 1974 (Ali, 1985). Australian-Friesian-Sahiwal (AFS) were introduced from Australia in 1983. Frozen semen of Holstein-Friesian and Jersey breeds from Australia, Germany, New Zealand and Kenya were introduced in 1987 and frozen semen of different genotypes such as Holstein-Friesian and Jersey were introduced from 1990 onwards coming from Australia, New Zealand, France and USA (Bhuiyan, 1997).

A breeding programme was established by the MOFL in 1982 to firstly breed cows for urban, semi-urban and milk pocket areas of 50% Friesian and 50% Sahiwal / indigenous composition, and secondly to breed cows for rural areas, of 50% Friesian and 50% indigenous breed composition. Some commercial farms also used 100% Friesian. However, this breeding policy was not satisfactory due to improper management and the low adaptability of Friesian crossbreds to local conditions (Bhuiyan, 1997). Therefore, the breeding policy was revised in late 1999.

The main change to the MOFL breeding programme was to emphasise traditional farming and the use of semen to improve the germplasm of indigenous cattle. In view of the national demand for milk, a new breeding policy is under formulation by the Ministry of Fisheries and Livestock through the Central Cattle Breeding Station (CCBS). The objectives of CCBS are to produce high quality semen from stud bulls and to disseminate this semen throughout the country via 22 AI centres, 423 AI sub-centres and 554 AI points (DLS, 2002). In addition, BMPCUL recently started their own breeding policy to improve the genetic merit of their members' cattle.

Figure 3.2: Animal shed of government dairy farm (Savar Dairy Farm)

3.2.2 Cattle feeds and feeding

The cattle of Bangladesh are principally fed on agricultural by-products such as crop residue and straw. Paddy straw, shrubs, tree leaves and twigs may also be fed to cattle. Sometimes cows with calves are kept tethered outside the house. Farmers graze their cattle during the daytime on natural pastures on non-arable land including public wasteland found around canals, rivers, roadsides and railways. Generally no arable lands are used for fodder cultivation (DLS, 2002).

Commercial farmers and the farmers supplying BMPCUL cultivate both perennial and seasonal fodder such as Napier, Corn, Cowpea and Keshari (Lathyrus Spp.). They also feed their cattle concentrates such as brans, oilcakes and some grains. The governmental dairy farms (Figures 3.2 and 3.3) cultivate different kinds of perennial and seasonal grasses and sometimes cattle are allowed to graze in fodder fields. Cattle are provided with silage and hay during off-seasons and concentrates throughout the year (Hossain, 2006).

Figure 3 3: Fodder field under government dairy farm (Savar Dairy Farm)

3.2.3 Processing and marketing of milk and milk products

It is estimated that about 3% of the milk produced in Bangladesh flows through the formal channels of processing (Hemme et al., 2004). The remaining 97% is informally handled as liquid milk through small traders (locally called Farias) and distributing traders (locally called Paikers) as shown in Figure 3.4. For marketing, small scale producers sell their milk directly to the end consumers. The middle- man collects milk from some commercial farmers and some small-scale producers and sells it on to retailers, who sell it to consumers.

In the cooperative system, BMPCUL ensures a regular collection of milk from their cooperative members. After collection, raw milk is transferred to processing plants for pasteurisation and packaging. The packaged milk is then sold to the distributor and the distributor sells it to the end consumers.

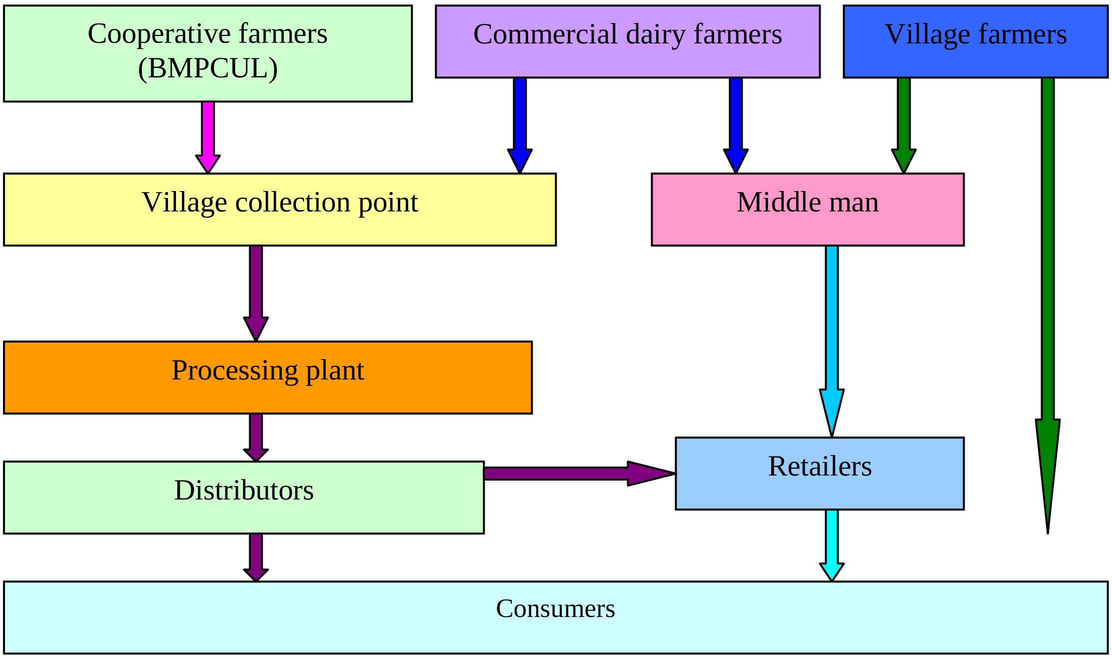


Figure 3.4: Processing and marketing of milk and milk products in Bangladesh

3.2.4 Breeding, production and marketing system under cooperative dairying in Bangladesh

The Bangladesh Milk Producers Cooperative Union Limited (BMPCUL), using the brand name Milk-Vita, incorporates member farms situated between 24°01′ and 24°47′ north latitudes and between 89°15′ and 89°49′ east longitudes. The member farms fall within a region that is surrounded by the rivers of Padma, the Jamuna, the Boral and the Chalon bill. Heavy silt deposited by these rivers during the rainy season continuously enriches the alluvial soil (Hossain, 2006). The area managed under BMPCUL is subject to a monsoon climate. The maximum temperature recorded in the summer months (mid-April to mid-June) is 37°C. Winter normally lasts from December to late February with temperatures between 7°C and 20°C. The monsoon season commences towards the end of June and continues until September. The level of rainfall is highest during the monsoon season and lowest in March, when demand for irrigation from tube-wells in the area peaks (Bangladesh

Meteorological Department, 2005). These climatic conditions provide an area that favours animal production.

Bangladesh Milk Producers Cooperative Union Limited (BMPCUL) is a large dairy cooperative, has around 40,000 small-holder dairy farmers who joined as members of around 345 primary dairy cooperatives. BMPCUL covers about 925 villages in 15 districts of Tangail, Manikgonj, Tekerhat, Baghabarighat, Sree Nagar and Rangpur areas.

3.2.4.1 Breeds and dairy cattle improvement programme under BMPCUL

The members of this cooperative societies milk Pabna cattle (a local variety; Figure 3.5), and its crosses with Sahiwal and Red-Sindhi breeds. In the greater Pabna district, two cattle production systems have been identified: a draught–oriented system with local Deshi cattle and a more milk-oriented production system using the Pabna milking cow (PMC) (Hermans et al., 1989; Udo et al., 1990). The PMC originated from crossing Deshi cattle with Sahiwal, Hariana and Red-Sindhi bulls. One of the major differences between the two production systems is that PMC have access to grazing lands along the rivers. Pabna milking cows are concentrated in the milk-shed area from where the cooperative dairy industry has formed.

The Bangladesh Cattle Development Project (BCDP) has attempted to increase milk production in some parts of the Baghabarighat milk shed area (where BMPCUL is situated) by introducing improved pasture management, health care and nutritional supplementation. Some exotic crossbred cows have also been introduced in order to evaluate their performance under traditional systems of management (Ahmed and Islam, 1987 and Bhuiyan and Sultana, 1994). They found that the crossbred showed higher performance in one generation and become worse in subsequent generations with high calf mortality. During 1990 to 1991 BMPCUL has created its own breeding station and in their bull-station. Sahiwal, Red-Sindhi, Pabna cattle, Holstein-Friesian and Jersey bulls are available and in addition, frozen semen of Holstein-Friesian and Jersey breeds from Australia, Germany and New Zealand is also available.

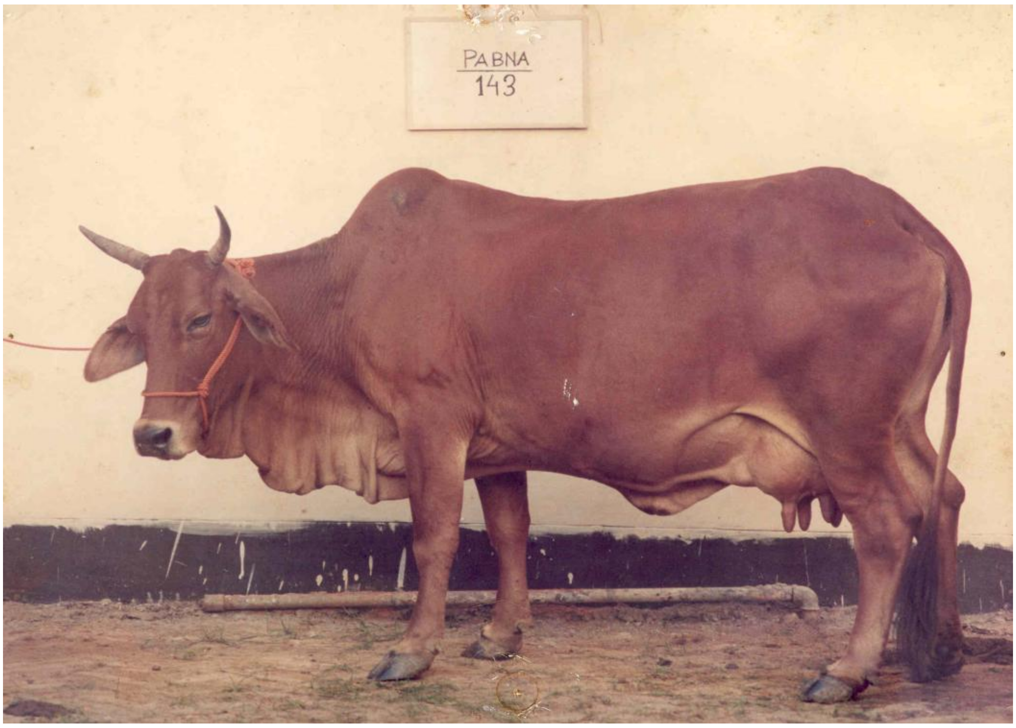


Figure 3.5: A typical Pabna cow (Source: BLRI, Savar, Dhaka)

3.2.4.2 Dairy production systems under BMPCUL

Within the Bangladesh cooperative dairying structure, dairy production systems can be classified based on the scale of production: small, medium or large. Large-scale production is fully commercial, while small-scale and medium-scale operations range from predominantly subsistence to largely commercial. In all three production systems, Pabna cattle, Sahiwal, and the crossbreds of Sahiwal, Hariana, Red-Sindhi, Holstein-Friesian and Jersey are used. The medium-scale and large-scale producers generate their own female replacements and breed their cows from semen produced by BMPCUL.

Some male calves are sold after weaning but most male calves are castrated and used for draft. The culled cows and surplus heifers are sold for slaughter.

Figure 3.6: Pabna cattle and local Deshi cattle are grazing on Bathan land (Source, BLRI, 2000)

3.2.4.3 Feeding and management of dairy cows

Generally, all calves are fed colostrum during the first 3 to 5 days and then approximately 0.5 to 1.0 kg of whole-milk is fed three to four times daily for a period of approximately 2 to 3 months (Hussain, 1987). Thereafter, and up to weaning at about 70 kg, they are fed whole-milk with roughage, and concentrate supplements. From weaning to age at first calving heifers, are offered concentrate, roughage and are grazed on natural pastures. From December to May, almost all cattle are grazed on natural pasture land named Bathan (Figure 3.6.). Feed from the Bathan provides about 1/3 of the feed required for the whole year (Islam and Bhuiyan, 1997). During the wet season, from June to November (Figure 3.7), cattle are fed mainly paddy straw and hay made from surplus grass; some farmers make silage. It is assumed that throughout the year, intake consists of about 2% silage and hay, 25-30% pasture and 70% paddy straw (Hossain, 2006).

Cows are grazed on natural pastures and during the dry period, approximately 5 kg of fresh weight green grass and 5kg of paddy straw are offered per cow per day. The lactating cows are fed a concentrate mix of approximately 2-3 kg/day. The concentrate mix includes rice polish, wheat bran, oilcakes and common salt (Hossain, 2006).

Figure 3.7: Pabna cattle and its crossbreds are in stall feeding condition during wet season

Other management practices, such as drenching, dipping, vaccination and de-worming are undertaken on most farms. Cows are culled and slaughtered when they are approximately 10 years of age.

In cooperative dairying, the farmer members pool their milk at the primary dairy cooperative societies, which arrange regular cash payment on the basis of milk volume and fat content. BMPCUL ensures milk collection from the primary cooperative and provides necessary support services to farmer members for animal breeding, feeding, health and training in animal management. A major part of the surplus earned by the central dairy cooperative through marketing milk and milk products is paid to its members.

3.2.4.3.1 Bathan and Bathan management

The Baghabarighat milk shed area is well known for its large “Bathan” areas and fertile lowland. Bathan is a basin-like area along the river Boral in the Pabna and Sirajgonj districts. About 600 hectares of land are used for the cultivation of Napier (*Pennisetum purpureum*), Jamboo, Shama (*Copsyhus cebuensis*) and seasonal legumes such as Matikalai, Keshari kalai, natural Durba (*Cynodon spp.*), Bermuda

(*Cynodon dactylon*) and Baksha (*Hemarthria altissona*). Black gram (*Vigna mungo*) and grass pea (*Lathyrus sativum*) are the major forage species usually broadcast into silt deposited by the departing monsoon flood in this Bathan area when the soil conditions are suitable. Farmers usually cultivate these legume species without tillage.

The great poet Rabindranath Tagore (Nobel Laureate) was the original owner of this land. In 1890 he declared that the Bathan land would be used for pastureland, not crop agriculture, and donated the entire area to the government. Poor and marginal farmers were allowed to cultivate green grasses and to graze their cows on this land (Hossain, 2006).

The milk producing cooperative use this land under the proper authority of the deputy commissioner, Sirajgonj. BMPCUL pays 500 Taka per year per 0.40 hectare of Bathan land to the Assistant Commissioner (land) in the Upa-Zila level. Cooperative members use this land under the control of the managing committee of the milk producing societies. Good management procedures are being followed with the cultivation and utilisation of green grasses in this Bathan land. During "Bathan" feeding, animals are kept in the field and managed by cow boys. Artificial insemination, parturition, vaccination, treatment and milking of animals are routine while animals are on the "Bathan".

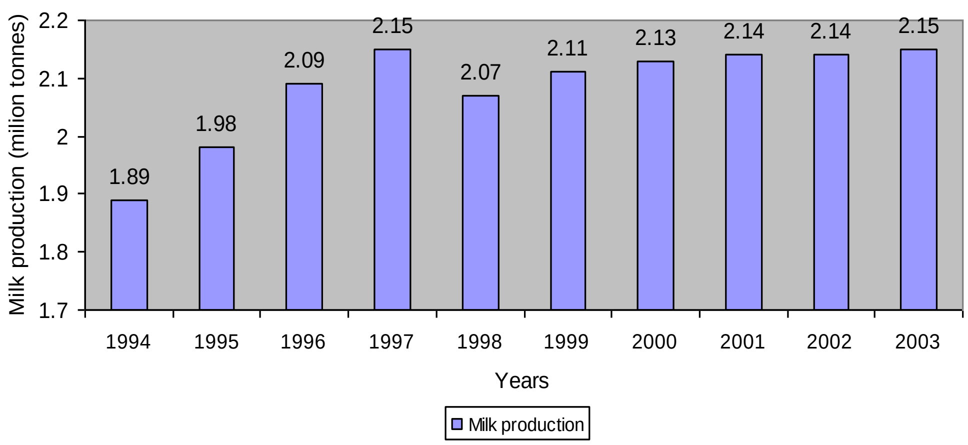
3.2.5 Production and demand for milk throughout the year

There is a great shortage of milk and meat production in Bangladesh (Figure 3.9); this shortage is primarily due to the low production of cows. Based on the estimate that the 141 million people in Bangladesh should each consume at least 120g of milk per day (as fluid or processed in any form), the annual milk demand should be about 6.13 million tons (FAO, 2004). This estimate of the national milk demand is over 25% of FAO's recorded national milk production for the country (FAO, 2004). To meet the shortfall, Bangladesh imports milk from developed countries at the expense of hard-earned foreign currency. Therefore, meeting Bangladesh's demand for milk is a huge national task.

The main reason for the failure to meet national milk demands is that the average milk yield per cow reported for Bangladesh is extremely low. On average, a Deshi cow produces around 206 kg/year (Ali and Ali, 2003), which is less than 30 percent of the production of Indian cows. The main reasons for low cow milk productivity are low genetic potential, feed shortage and high incidence of disease. This low productivity could be improved with proper and efficient planning of the whole industry, and would require consistent and objective breeding decisions.

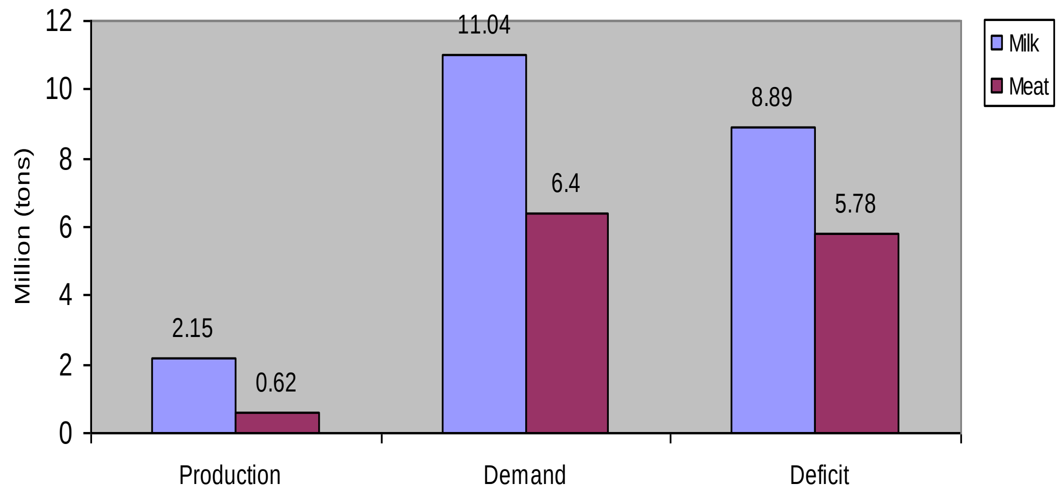
The yearly milk production (million metric tonnes) of Bangladesh from 1994 to 2003 is presented in Figure 3.8. Bangladesh has seen a slight improvement in milk yields over the period from 2000 to 2005 (FAO, 2006). This increase is due mainly to the importation of temperate germplasm and keeping them for 2 to 3 lactations and also to the importation of live animals from India. The majority of animals, which are local cattle breeds, increased their milk yield by around 5 percent over this period, while the milk yield of crossbred cows increased by 4 to 8 percent (DLS, 2002).

Figure 3.8: Yearly total milk production of Bangladesh (FAO, July, 2004)



About 64% of the country's milk is cattle milk, with goats contributing 35% and buffalo 1% to national milk production (Hemme et al. 2004) Bangladesh produces 0.35% of the total world milk production. This represents about 8% and 2% of the milk production of Pakistan and India respectively, or 1.75% of the milk production of South Asia.

Figure. 3.9: Production demand and deficit of milk and meat (DLS,2000)



3.2.6 Summary

- In Bangladesh dairy cattle production is mainly integrated with crop farming, but there are nine governmental farms, approximately 56,000 commercial dairy farms, and a large central dairy cooperative, BMPCUL.

- The farmers of Bangladesh feed their cattle mainly paddy straw, however some seasonal legumes and perennial grasses are given, especially by commercial and cooperative farmers.

- The marketing and processing systems are traditional, but under BMPCUL this system is more organised.

- There is a big difference between the production of, and demand for, milk in the country.

- Increases of milk yield could be possible with successful artificial insemination using semen from high genetic merit bulls and the number of animals increased through the importation of live animals from neighbouring countries.

3.3 Crossbreeding

Crossbreeding experiments have been conducted on government dairy farms in Bangladesh since 1970 and consequently, both purebreeding and crossbreeding systems are being used by dairy farmers (Ahmed, 1985). The majority of cattle in Bangladesh are zebu type (Bos indicus), but the present cattle improvement programme seeks to improve indigenous cattle by utilising both tropical and temperate breeds.

3.3.1 Productive and reproductive performances of crossbreds

The productive and reproductive performance of different genotypes of cattle in Bangladesh, has been studied by a number of researchers (Ahmed and Islam, 1987; Nahar et al., 1992; Hirooka and Bhuiyan, 1995; Islam and Bhuiyan, 1997; Bhuiyan et al., 1998; Majid et al., 1998; Khan and Khatun, 1998; Khan et al., 2000; Hossain et al., 2002; and Islam et al., 2004). These authors collected productive and reproductive performance records from governmental, cooperative and private dairy farms in Bangladesh. Data was analysed using statistical models suggested by Steel and Torrie, (1980) and Steel et al. (1997) to compare the performances of various genetic groups of animals. A summary of the results is presented in Table 3.1.

Local crossbred cows were reported to have lower milk production, longer calving intervals, and later sexual maturity compared to Holstein-Friesian (HF) and HF crosses. However, low survivability of temperate breeds (e.g. Ayrshire) in tropical environments has been reported relative to crosses of tropical breeds like Sahiwal and Red-Sindhi with local cattle (Table 3.2; McDowell, 1985; Cunningham and Syrstad, 1987; Rege et al., 1998; and Kahi et al., 2000).

Table 3.1 also indicates that age at sexual maturity and calving intervals, differ between Sahiwal and Holstein-Friesian. It is commonly reported that reproductive performance differs between breeds and the crossbreds of *Bos taurus* with *Bos indicus* in the tropics (Syrstad, 1989, 1990; Madalena et al., 1990; Sharma and Pirchner, 1991; Thorpe et al., 1993, 1994; Rege et al., 1994, 1998 and Kahi et al., 2004).

Table 3.1: Productive and reproductive performance of different cattle breeds in Bangladesh

Trait	Genetic Group						
	L	P	S	H	S×L	S×P	H×L
Birth Weight (kg)	14[3]	-	-	27[3]	18[4]	21[9]	17[3]
	16[6]	-	-	-	21[10]	-	21[4]
Age at sexual maturity	1140[5]	687[5]	1080[5]	659[5]	1059[4]	1118[8]	920[4]
(days)	-	-	-	-	-	1156[9]	990[10]
Calving interval (days)	484[5]	450[5]	502[5]	493[5]	479[4]	-	470[4]
Gestation period (days)	279[5]	283[5]	279[5]	283[5]	279[5]	286[8]	279[1]
	-	286[8]	-	-	280[4]	285[9]	280[4]
Service per conception	1.76[5]	1.29[5]	1.90[5]	1.27[5]	1.08[8]	-	1.18[10]
	-	1.20[8]	-	-	1.09[9]	-	-
Mature liveweight (kg)	234[6]	-	295[7]	395[7]	-	-	-
Daily milk yield (kg)	2.4[2]	3.5[5]	3.24[2]	10.3[3]	3.18[2]	8.0[8]	6.5[3]
	2.93[3]	-	-	-	2.9[4]	8.37[9]	5.5[4]
	1.8[6]	-	-	-	-	8.0[10]	9.7[10]
Lactation production	540[2]	735[5]	877[2]	2900[2]	726[2]	1738[8]	1703[4]
(kg)	386[6]	-	-	-	870[4]	2018[9]	1866[10]
						1738[10]	
Lactation length (days)	222[2]	209[8]	254[2]	290[2]	235[2]	214[8]	330[4]
	214[6]	210[5]	-	-	296[4]	217[9]	207[10]

L= Local Bangladesh, P=Pabna cattle, S = Sahiwal, H= Holstein-Friesian

[1]Islam et al.,2004; [2]Hossain et al., 2002; [3]Hirooka and Bhuiyan, 1995; [4] Nahar et al.,1992; [5] Majid et al.,1998; [6] Khan et al., 2000; [7] Ahmed and Islam,1987; [8] Khan and Khatun,1998; [9] Bhuiyan et al.,1998.[10] Islam and Bhuiyan, 1997.

Table 3.2: Survivability (%) in different age groups of Sahiwal, N'Dama, Ayrshire, African Zebu, Jersey × N'Dama, Friesian × Tharparkar and Friesian × Sahiwal genotypes in India and Ivory Coast

Age	Genotypes							
	Purebred				Crossbreds			
	S	N'D	AZ	A	J×N'D	F×S	F×T	¼ F×S
0-3 months	-	91(1)	-	-	92(1)	-	94(2)	-
0-Adult	86(1) 72(1)	-	95(1)	83(1)	96(1)	96(2)	-	67(2)

S= Sahiwal; N'D= N'Dama; AZ=African Zebu; A = Ayrshire; J= Jersey; F= Friesian; T= Tharparkar
(1)McDowell, 1985; (2)Cunningham and Syrstad, 1987.

Table 3.3: Productive and reproductive performance of different genotypes of cattle in tropical countries other than Bangladesh

Trait	Genetic group							
	F×B (F_1)	J×B (F_1)	A×S	F×S (F_1)	S×H	F×S (F_2)	J×Ha	F×Ha
Age at sexual maturity (days)	1080[(1)]	1050[(1)]	979[(2)]	967[(2)]	780[(4)]	-	540[(6)]	570[(6)]
Service per conception	1.49[(1)]	1.31[(1)]	-	-	-	-	-	-
Calving Interval (days)	417[(1)]	408[(1)]	412[(2)]	441[(2)]	-	338[(5)]	-	-
Days open (days)	133[(1)]	123[(1)]	-	-	-	-	-	-
Daily milk yield (kg)	-	-	5.4[(2)]	5.6[(2)]	-	10.8[(5)]	6.2[(6)]	6.3[(6)]
Lactation length (days)	-	-	313[(2)]	290[(2)]	305[(4)]	320[(5)]	304[(6)]	345[(6)]
Lactation production (kg)	-	-	3019[(3)]	1611[(2)]	5142[(4)]	3922[(5)]	1898[(6)]	2162[(6)]

F = Friesian; B= Boran; J= Jersey; A= Ayrshire; R= Red Sindhi; H= Holstein-Friesian;
S= Brown-Swiss; and Ha= Hariana

(1)Demeke et al., (2004); (2)Thorpe et al., (1993); (3)Thorpe et al. (1994); (4)McDowell and McDaniel, (1968); (5) Kahi et al., 2000 and (6)Guha, 1968 (cited in Anon, 2004).

The productive and reproductive performance of cows from other tropical countries is presented in Table 3.3. Holstein-Friesian crossbreds show better performance such as early age of sexual maturity and high lactation production than other crossbreds.

3.3.2 Economic evaluation of crossbreeding in tropics

The majority of work on cattle crossbreeding in the tropics, including Bangladesh, has been biological, involving comparisons of productive and reproductive performances. Some economic evaluations of crossbreeding strategies have been conducted under temperate conditions (e.g. McDowell and McDaniel, 1968; Touchberry, 1992; McAllister et al., 1994 and Lopez-Villalobos et al., 2000). However each report has used a different criterion which affects the outcome of the comparison (Kahi et al., 1998). For example, a number of authors from tropical regions considered only returns on milk and manure sales, and the costs associated with milk production in their economic evaluation (Ram and Singh, 1975; Patel et al. 1976; Parmar and Dev, 1978; and Kanchan and Tomar, 1984). In contrast, other authors have used a profit function that, in addition to milk sales, includes returns from sales of calves and culled cows (Reddy and Basu, 1985; Madalena et al., 1990). Madalena et al. (1990) concluded that the maximum profit was obtained by utilising F_1 Holstein-Friesian cross Guzera heifers over a wide range of economic simulations.

Economic evaluations of crossbreeding in tropical environments are presented in Table 3.4. Pure Holstein-Friesians showed a higher profit than all crossbreds examined (Madalena et al., 1990; Gunjal et al., 1997; Kahi, et al. 2000). Of the crossbreds evaluated, the Holstein–Friesian × Sahiwal combination was found to be superior to other genetic combinations in terms of profitability (Kahi et al., 2002). Estimation of the profit from Holstein-Friesian × Ayrshire cows indicated that maximum profit was obtained by utilising F_1 rather than other proportions of inheritance (Gunjal et al., 1997).

Table 3.4: The economic evaluation ($ per day) of different dairy cow genotypes in tropical countries

Parameters	Genetic Group			
	H [1]	H × S[2]	H × A[1]	H × Guzera[3]
Milk revenue	6.67	1.84	5.54	-
Calf revenue	0.35	0.36	0.34	-
Other revenue	2.38	-	2.02	-
Total revenue	9.40	2.20	7.90	-
Feed cost	3.96	0.55	3.39	0.304
Health cost	-	0.043	-	-
Labour cost	1.68	-	1.54	0.043
Reproductive cost	0.12	0.0105	0.10	-
Profit	3.64	1.60	2.87	1.79

H = Holstein-Friesian; S = Sahiwal; A = Ayreshire;

[1]Gunjal et al., 1997; [2]Kahi et al., 2000; [3]Madalena et al., 1990.

3.3.3 Summary

- Crossbreeding experiments in Bangladesh have focussed on biological rather than economic evaluations.
- Holstein-Friesian combinations are better for both productive and reproductive traits than the other breed combinations.
- Due to the lower survivability rate of Holstein crossbreds in the tropical environment, the Sahiwal breed is preferable to other breeds, although further study is required on survivability.
- The productivity of crossbreds is higher than the purebreds and so incorporating a crossbreeding programme will inevitably help increase profit, but further work concentrating on economic aspects is required to confirm this.

3.4 A survey of dairy production under cooperative dairying

3.4.1 Collection of experimental data

During the period of June to September 2005, 50 farm households were surveyed by interview with a questionnaire designed for the collection of data on production, processing and marketing of milk products under the cooperative dairying system in Bangladesh (Appendix 1)

Based on the International Farm Comparisons Network methodology (IFCN, 2002), three farm types were identified as "typical". These are:

BD-2: This type of farm represents a rural household with an average of two local cows and 0.4 hactare of land. The farm sells about 60% of its milk to the local milkman. This type of farm represents the majority of farms in Bangladesh.

BD-10: This type of farm is located in a rural area and has an average of 1.6 hactare of land used for growing small grain crops. Up to ten dairy animals are kept. Ninety percent of the milk is sold to a nearby milk collection point. The household depends on the farm as its sole source of income.

BD-25: The rural farm has an average of 1.8 hactare of land and keeps up to 25 crossbred cows. The majority of milk (98%) is sold to a milk processing company at a collection centre nearby.

In the survey, the number of animals kept per farm ranged from 25 to 180. Although this size of dairying unit is not typical in Bangladesh, they are common in cooperative areas especially in the Baghabarighat milk shed area.

3.4.2 Results and discussion

3.4.2.1 Breed and age groups

Generally, farms in the Baghabarighat area have herds consisting of the following breeds: Pabna cattle, Sahiwal, Holstein-Friesian and the crossbreds of Sahiwal × Pabna and Holstein-Friesian × Pabna, Holstein-Friesian × Local and Jersey × Pabna (Khan Survey, 2005). Some households farmed Australian-Friesian × Sahiwal cattle. Usually, the dairy herd is of mixed breed and the farmers keep most of the available breed types.

The breed composition of the surveyed farms, and the percentage of the different genotypes of cows by age group in the BMPCUL areas are shown in Tables 3.5 and 3.6, respectively. The proportion of cows with Holstein genetics is greater than all other genotypes combined. This is probably due to the fact that cows with Holstein genetics produce higher milk yield than local and other crossbreds. Therefore, the farmers in BMPCUL areas prefer to rear Holstein and its crossbreds.

Table 3.5: Breed composition on cooperative dairying farms in Baghabarighat milk-shed area from a survey of 50 farms

Genotype	Total Number	Percentage of total	Milking Cow number	Percentage of milking cows
Pabna	363	13.2	144	39.7
Sahiwal	67	2.4	25	37.3
Holstein Friesian	78	2.8	30	38.5
Sahiwal × Pabna	525	19.0	197	37.5
Holstein- Friesian × Local	449	16.3	170	37.9
Holstein-Friesian × Pabna	773	28.0	309	40.0
Holstein- Friesian × Sahiwal	306	11.1	116	38.0
Sahiwal × Holstein-Friesian	29	1.1	11	38.0
Jersey × Pabna	53	1.9	19	36.0
Other (Non-descriptive)	105	4.2	40	65.0
Total	2748	100	1061	

Table 3.6: Age distribution of milking and dry cows (number) within breed from a survey on 50 cooperative dairy farms in Bangladesh

Genotypes	Age (Years)								Total
	4	5	6	7	8	9	10	10+	
Pabna	2	4	10	32	28	26	36	6	144
Sahiwal	4	-	-	3	2	11	4	1	25
Holstein-Friesian (HF)	-	-	3	15	8	3	1	0	30
Sahiwal × Pabna	1	7	18	37	63	42	24	5	197
HF × Local	2	6	20	31	42	56	13	0	170
HF × Pabna	4	5	12	16	28	25	20	6	116
HF × Sahiwal	12	25	33	57	66	70	36	10	309
Sahiwal × HF	-	-	-	3	5	2	1	0	11
Jersey × Pabna	-	5	1	8	3	2	0	0	19
Total	25	52	97	202	245	237	135	28	1021
Percentage of total	2.45	5.09	9.50	19.78	24	23.21	13.22	2.74	

From Table 3.6, it can be seen that the Holstein crossbreds appears to have higher survival rate than other genotypes. But farmers purchase this genotype and keep them for beef production. If the cows give birth they produce more milk than the local genotypes but in terms of costs and benefit this genotype is not profitable after 2 to 3 lacations. Generally, temperate breeds and their crossbreds including Holstein genotypes maintain only 2 to 3 lactations because of lower productivity due to poorer adaptability. The low productivity and poor adaptability of temperate breeds and their crossbreds in tropical environment has also been reported in several other studies (e. g. Cunningham and Syrstad, 1987; Madalena, et al., 1990; Syrstad, 1989, 1990, 1996; Rege et al., 1993, 1998; and Kahi et al., 2002).

The farmers in BMPCUL areas are more business-oriented than other parts of Bangladesh, so they maintain their cows production to almost maximum levels. The cows give birth at an average of 4 years of age and usually the farmers cull cows after 10 years. This is consistent with reports that throughout Bangladesh, more than 60% of milking cows are less than 10 years of age (BBS, 1999). Sometimes cows are kept for milk and draught power after this age, if they continue to produce adequate milk.

3.4.2.2 Housing

During the months of June to November the cattle are usually kept under stall feeding conditions. All breeds and age groups are kept in unplanned semi-intensive housing for 24 hours per day. However, calves, heifers, cows and bulls are kept separately in different locations. Overall sanitation of each farm was good with routine cleaning and washing activities carried out every day. It has been recommended that a milking cow requires 100 square feet indoors, while a calf requires 25 square feet, and a growing cow 30 to 40 square feet (Hossain and Akhter, 1999). However, the farmers surveyed could not always provide the required space per animal during stall feeding conditions.

3.4.2.3 Feeds and fodder

Feeding and management systems of cows in the Baghabarighat Milk Shed area were found in two categories: one as “Bathan” feeding in the dry season (November to May) and the other as stall feeding during the rainy season (June to November). The results of the survey revealed that cows in this area were fed 4 to 5 kg straw and 2 to 3 kg concentrates throughout the year. The concentrate mix contained sesame oil cakes, coconut oil cakes, wheat bran, rice polish, keshari bran, grams bran, mashkalai brans and common salt. During the rainy season the farmers fed their animals with concentrates and fodders, with a small amount of green grass. During the dry season, milking cows usually graze on the Bathan area on a pasture rotation system. Usually, farmers divide the pasture into 3 to 6 paddocks with temporary fences and cattle are moved systematically from one paddock to another on a rotation basis. Each paddock is grazed for a period of 7 to 14 days, the period being dependent on stocking rates and herbage growth.

3.4.2.4 Liveweight

Body length and the heart girth were measured in inches using a measuring tape and the liveweight of each cow was calculated according to the method of Hossain and Akhter (1999) as follows:

$$\text{Live weight (kg)} = \frac{\text{Body length} \times (\text{Heart girth})^2}{300 \times 2.2}$$

The estimated mature (6 to 7 years old cows) liveweight of the different genotypes of cow in the Baghabarighat milk shed area is shown in Table 3.7. Holsten-Friesian cows show a higher liveweight and Pabna cows were lighter with all other genotypes being intermediate. The estimated liveweight of all the genotypes was similar to that reported in other studies (e.g. Khan et al., 2005; Ahmed and Islam, 1987).

3.4.2.5 Milk production characteristics of different genotypes

There is no well-developed recording system for the productive and reproductive traits of cows in the BMPCUL cooperative area. However, the farmers keep records of milk payment from BMPCUL. Data on lactation length (days) and lactation production (kg) were calculated from the farmers' record books for the previous year (2004). Days in milk was defined as the number of days from parturition up to the day of survey and was estimated based on farmer interviews, as well as some supplementary information from their record books.

The milk production characteristics of the current lactation number, including the daily milk yield (kg), days in lactation, lactation length (days) and estimated lactation production (kg) of different genotypes of cattle are shown in Table 3.7.

The lactation production was calculated as the product of the daily milk yield, and the lactation length in days. The average daily milk yield, lactation length and therefore lactation production of Pabna cattle was lower than the other breed and crossbreds (Table 3.7). The Holstein and it's combinations produced the greatest amount of milk although these cows had similar lactation lengths to other types of cows. This meant that Holstein purebreds and crossbreds had higher lactation production than other cows (Table 3.7). Similar findings were reported by other researchers (Hossain, 2006; Khan and Khatun, 1998 and Khan et al., 2005).

The lactation number of Holstein cows was lower than Sahiwal and Pabna because the farmers usually only keep the Holstein and its crossbreds for 2 to 3 lactations. After this age their productivity and survivability decreased. This might be caused by breed effects and also the genotype × environment interactions. On the other hand, Pabna and Sahiwal cows were kept for more lactations than Holstein genotypes, as they are adapted to the local environment and are more disease resistant.

The availability of milk and numbers of cows (milking) throughout the year is shown in the Figure: 3.10 and 3.11. There is a trend towards higher milk yield during the months of November to May. This is likely caused by improved energy balance when cows are grazed on the ample fresh grass available during these months and also for the number of increased milking cows. For similar reasons the number of milking cows also increased in this period (Figure 3.10.).

Figure: 3.10. Number of milking cows per house throughout the year at Baghabarighat milk shed area

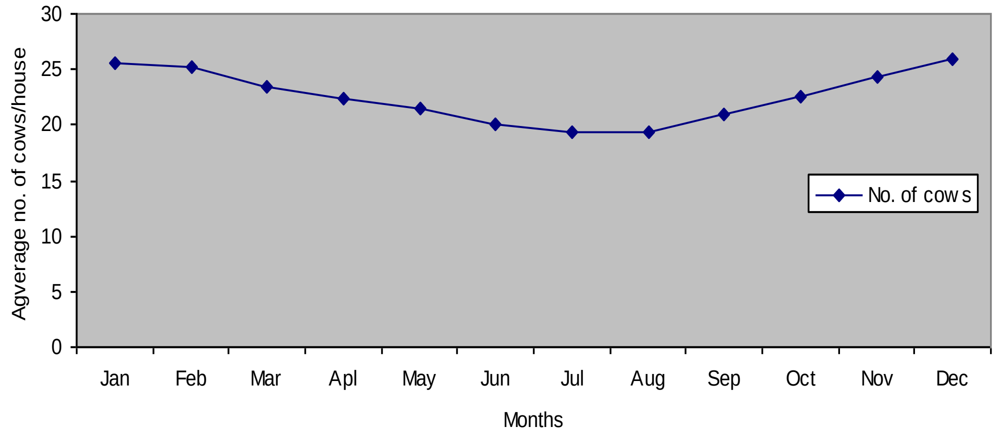


Figure 3.11. Milk yield (tonnes) per house throughout the year at Baghabarighat milk shed area

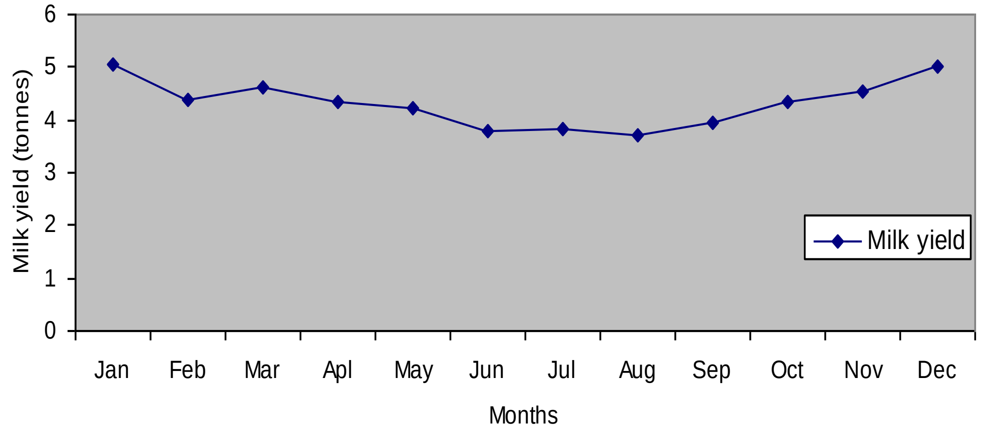


Table 3.7: Estimated milk production characteristics and mature liveweight (±SE) of different genotypes under BMPCUL area

Traits	Genotypes							
	P	S	H	S × P	H × L	H × P	H × S	J × P
Lactation No	3.23 ± 0.19	3.54 ± 0.58	1.56 ± 0.18	3.03 ± 0.13	2.19 ± 0.11	2.22 ± 0.08	2.50 ± 0.18	2.29 ± 0.35
Daily Milk Yield (kg)	5.22 ± 0.13	6.29 ± 0.39	7.56 ± 0.67	6.91 ± 0.16	7.10 ± 0.20	7.26 ± 0.17	7.93 ± 0.25	6.68 ± 0.50
Days in Lactation	164.33 ± 4.80	175.42 ± 10.70	168.75 ± 12.68	165.89 ± 4.26	169.24 ± 5.24	167.48 ± 3.7	166.15 ± 5.09	151.43 ± 19.28
Lactation Length (Days)	271.72 ± 2.27	266.67 ± 5.95	274.29 ± 4.79	271.30 ± 2.25	265.59 ± 2.72	265.48 ± 1.8	268.2 ± 3.33	299.45 ± 4.20
Lactation Production (kg)	1418.38	1677.35	2073.63	1874.64	1885.69	1927.38	2126.83	2000.33
Liveweight (kg)	246.8 ± 4.6	315.5 ± 4.9	444.5 ± 7.5	306.8 ± 4.4	379.1 ± 4.5	372.6 ± 3.7	386.3 ± 6.5	307.4 ± 4.9

Legends: S= Sahiwal, H= Holstein-Friesian, J= Jersey, P = Pabna, L = Local

3.4.2.6 Survivability of different breeds under cooperative dairying conditions

The primary reason for culling animals from herds was reported to be disease, low production and reproductive failure. Other reasons given included sale of stock for cash to meet the farmer's yearly family expenditure, and to enable the purchase of land or other livestock. Farmers experienced reduced income due to low production from the infected cows. The main pathogenic diseases found in the cooperative areas were reported to be foot and mouth disease, mastitis, hemorrhagic septicaemia, black quarter, anthrax and brucellosis (Khan Survey, 2005). Every year more than 20% of the dairy cows under cooperative dairying suffer foot and mouth disease (Uddin, 2004). The main non-pathogenic health issue was the retention of the placenta following parturition.

Farmers in the BMPCUL area reported regularly vaccinating their animals against disease (foot and mouth disease, black quarter, anthrax and brucellosis). Regular vaccination, de-worming and treatment are provided by veterinary surgeons working for BMPCUL. Farmers are charged 0.60 Taka per kg of milk supplied to the cooperative for the cost of animal health services.

Information on the survivability of different genotypes of dairy cattle in Bangladesh, was collected during farmer interviews and also from the literature (e.g. Shamsuddin, et al. (2006; Khan et al. 2005 and Debnath et al. 1995); and the combined results being shown in Table 3.8. Holstein and its crossbreds were reported to have lower survivability than Pabna and Sahiwal cattle. The causes may be genotypes × environment interactions. Similarly, low survivability of temperate breeds and their crossbreds in a tropical environment was reported by McDowell (1985) and Cunningham and Syrstad (1987).

Table 3.8: Survivability (%) of different genotypes of dairy cattle in Bangladesh

Stages	Genotypes							
	P	S	H	S×P	H×P	H × L	H×S	J × P
Calves	81	88	70	76	78	74	73	75
Heifer	92	90	90	91	82	86	88	85
Bull	92	92	94	90	88	90	92	90
Cow	92	90	90	93	87	91	86	90
Bull	96	96	99	98	93	95	95	96
Overall	91	91	89	90	86	87	87	87
0 to adult	88	89	83	87	82	84	82	83

Legends: S= Sahiwal, H= Holstein-Friesian, J= Jersey, L = Local and P = Pabna

3.4.2.7 Breeding

The farmer members of the BMPCUL, reported that they typically use artificial insemination; however, sometimes they use a bull for natural service. About 80% of farmers reported using artificial insemination (Hossain, 2006). From the current survey, about 60% of the farmers prefer a Sahiwal sire because of higher milk production with less disease susceptibility, together with a higher number of lactations per lifetime. About 40% of the farmers preferred Holstein and Jersey sires to improve their cattle, with the major reason for choosing the Holstein breed, being the substantial increase in milk production.

3.4.2.8 Processing and price of milk

The farmers in the cooperative area mostly produced raw milk, while some produced yoghurt. The price per kg of milk varied from 15 to 18 taka, with an average of 16.5 taka recorded in 2005. The fat percentage of individual farmer member’s milk is measured by BMPCUL staff, and the price of milk for cooperative members varies on the basis of fat content. These prices were based on milk with 4.5% fat. From 1000 ml of milk, farmers produced an average of 750 to 800 ml yoghurt. The price per kg of yoghurt varied from 35 to 40 taka, with an average of 37.5 taka in 2005.

3.4.2.9 Dairy products

Dairy products available in urban centres of Bangladesh include pasteurised liquid milk, butter, ghee, ice-cream, ice lollies, full cream milk powder, skim milk powder, flavoured milk, sweet curd, cream and Rasa malai (sweetmeats). The market price of different dairy products is shown in Table 3.9. The prices vary between period, markets and producers and also on a product by product basis.

Table 3.9: Market prices of different dairy products in year 2005 (1 US$ = BDTaka 70)

Product	Price per kg (Taka)
Butter	150
Clarified butter (ghee)	500
Ice-cream	100
Rasa malai (sweetmeat)	150
Ice lollies /Ice bar	200-230

3.4.2.10 Labour

The 2005 survey indicated that dairy herds within the BMPCUL were managed by farm labourers. Generally one labour unit managed a herd ranging from 10 to 20 animals of various ages. Some labourers were paid on a daily basis but most of the labourers worked on an annual payment basis. The wages per labourer varied from 80 to 100 taka per day in 2005, depending on the age and experience of the labourer.

3.4.2.11 Farm economics

The economics of dairy production under the BMPCUL cooperative dairy structure was calculated from the field data collected in 2005. In this study, annual profit was derived as the difference between revenue (R) and costs (C). Annual profit is expressed through grouping terms by class of cattle and calculating revenue and cost per cow per year. The revenue (R) per cow per year was calculated using the equation:

$$R = R_{\text{calves}} + R_{\text{culled heifers}} + R_{\text{bull}} + R_{\text{milk}} + R_{\text{culled cows}}$$

Costs (C) were calculated using from the following equation:

$$C = (C_{\text{male calves feeding costs}} + C_{\text{male calves health costs}} + C_{\text{male calves marketing costs}} + C_{\text{heifer calves feeding costs}} + C_{\text{heifer calves reproduction costs}} + C_{\text{heifer calves health costs}} + C_{\text{heifer calves labour costs}} + C_{\text{cow feeding costs}} + C_{\text{cow health costs}} + C_{\text{cow reproduction costs}} + C_{\text{cow labour costs}} + C_{\text{marketing cost}} + \text{Fixed costs.}$$

Fixed costs include those attributable to equipment, machines and farm structures. Apart from these fixed costs, all other costs are variable, as they are influenced by the level of herd production. In this cost analysis, the bull rearing cost and milk marketing were not considered, as the stud bulls were reared by the BMPCUL bull station and the BMPCUL paid the milk payment to their members, after deducing service and marketing costs.

Table 3.10 provides a breakdown of the average revenue, expenditure and profit of dairy farmers included in the 2005 survey. The average number of cows per farm, for survey respondents was 23. Based on this number of cows, the analysis indicated that milk income provided 81% of the total revenue of dairy farming in the Baghabarighat milk shed area under BMPCUL. The total annual farm income in 2005 was calculated to be US$1257.70 for an average 23 cow dairy herd. This profit/income per farm was similar to that estimated for Bangladesh cooperative dairy farms by Hemme et al. (2004); they estimated the annual farm income to be between US$1,160 to US$3,680 in 2004.

Stock sale proceeds were calculated for all classes of stock: calves, heifers and bull calves. Rebates and others were calculated for culled cows and bulls.

Feed is the major constraint of dairy production, and throughout the year the farmers feed their cows concentrate mix. For this reason the feed costs for all animals accounted for about 80% of the total costs, and included the cost of both roughage and concentrates. Non-dairy expenditure (repairs and maintenance, bank interest and farm overheads), and animal health costs including treatment, vaccination and de-worming accounted for 2.0% and 4%, respectively. In the matter of labour, the

Table 3.10: Annual farm production characteristics, revenue and expenditure (in BD Taka) determined from BMPCUL farms in 2005 (1 US$ = Taka 70).

Trait	Per farm	Per cow	Per litre of milk
Milk production (kg)	51,832.5	2,300.6	-
Maximum cows milked	60		
Revenue			
Milk sale proceeds	845,591.1	37,522.8	16.3
Stock sale proceeds	123,594.3	5,483.3	2.4
Rebates and other revenue	77,038.2	3,417.8	1.5
Total dairy cash revenue	1,046,223.5	46,424	20.2
Total farm revenue	1,046,223.5	46,424	40.4
Dairy Expenditure			
Wages	79,596.4	3,531.3	1.5
Animal health	35,292.3	1,565.8	0.7
Breeding	6,087.4	270.1	0.1
Shed expenses	37,030	1,642.9	0.7
Pasture+ Straw	95,221.9	4,224.6	1.8
Concentrate	682,335.8	30,272.2	13.2
Total Dairy expenditure	935,563.7	41,506.8	18.0
Non dairy Expenditure			
Repair and maintenance	3703	164.3	0.07
Bank interest	5208	231.1	0.10
Total farm overhead	20000	887.3	0.39
Total farm expenditure	964474.7	42789.5	18.6
Cash surplus from farming	81,749.3	3634.5	1.6
Cash surplus from farming (US$)	1257.7	55.9	0.03

average wage rate per day of 110 Tk per labour was used, and the total of which accounted for about 8.0% of the total expenditure.

From the economic study it can be seen that the dairy farming under BMPCUL is profitable.

3.4.2.12 Major constraints for Bangladesh cooperative dairy operation

The major constraint for dairy production under the cooperative system was found to be access to feed of sufficient quality and quantity. This was especially so during the monsoon period, when farmers suffer from a shortage of green grass. Disease and parasitic infestations are the second most important constraint on dairying. Suitable breeds of cow for dairying, their artificial breeding, inadequate breeding programmes and capital (money) add further constraints on dairy farming and there are no well defined breeding objectives. The Holstein and its crossbreds are reported to produce the most milk; however, farmers only keep these genotypes for 2 to 3 lactations because of decreased survivability after this time. On the other hand, the Sahiwal, Pabna and Sahiwal × Pabna crosses are more adapted and feed efficient than temperate breeds although they produce less milk per lactation, the Pabna and/or Sahiwal breed and their crosses may be more suitable for milk production under these farming conditions.

3.4.2.13 Summary

- Fifty farm households that were members of the BMPCUL cooperative society in the Baghabarighat milk shed areas were surveyed in 2005. The herd size ranged from 25 to 180 animals.

- The herds of the survey respondents consisted of Pabna cattle, Sahiwal, Holstein-Friesian and the crossbreds of Sahiwal × Pabna and Holstein-Friesian × Pabna, Holstein-Friesian × Local and Jersey × Pabna.
- Data were collected for productive and reproductive traits. The highest daily milk yield and lactation yield were recorded for Holstein cows and Holstein crossbreds. However the Pabna and Sahiwal breeds produce a greater number of lactations, resulting in a higher lifetime milk yield from these breeds and their crosses.

- The survey revealed that about 60% farmers were interested in using Sahiwal sires and 40% in using Holstein and Jersey sires.

- The economic evaluation indicated that dairy farming under cooperative dairying was profitable.

3.5 Remarks

1. Bangladesh has a great shortage of milk and there is a national demand to increase milk production.

2. There is no well-developed recording system for dairy cattle genetic evaluation.

3. The major constraints for genetic improvement of dairy cattle in Bangladesh are ill-defined breeding objectives, inefficient artificial breeding programmes, small population size, and lack of infrastructure and skilled personnel.

4. In Bangladesh, research on estimating the genetic merit of available genotypes, economic evaluation of different breeds in different management schemes, and the genetic improvements programmes of dairy cattle is limited.

5. Bangladesh Milk Producers Cooperative Union Limited (BMPCUL) is a well-organised large cooperative dairy production system. Under this system, there exists the potential to organise a dairy cattle genetic improvement programme, in the future.

6. Data from the 2005 survey is used in subsequent chapters to: (a) model the lactation curves of different breeds in order to predict the total lactation yield from incomplete lactation records, (b) develop a dairy farm model and economic evaluations, (c) develop a breeding objective, and (d) develop a multitrait simulation model for total merit of dairy cattle.

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CHAPTER FOUR

Lactation Curves of Different Cattle Breeds under Cooperative Dairying Conditions in Bangladesh

4.1 Abstract

This study was undertaken to compare and evaluate the parameters of ten different mathematical models for their predictive ability in describing the lactation curves of different breed groups under cooperative dairying in Bangladesh. A database consisting of 7340 records, from 738 cows of Pabna cattle, Australian-Friesian-Sahiwal × Pabna, Holstein × Pabna, Jersey × Pabna, and Sahiwal × Pabna genotypes from the period 1999 to 2001 was used. The estimated parameters of the mathematical models, and the predicted lactation milk yields differed significantly ($P<0.05$) between genotypes, years, and seasons. The Ganies, Rook and Dijkstra equations did not fit the observed data, and were discarded from further consideration. The remaining models were evaluated by four goodness of fit statistics (AIC, R^2, RootMSPE and CCC). The AIC value indicated Ali polynomial regression, and Sikka models provided a good fit for all genotypes, but, the CCC and RootMSPE values for these models indicated a poorer low fit. The R^2 value suggested that the Legendre polynomials and Wilmink models were the best fit for all genotypes. CCC and RootMSPE values indicated that the best models were Nelder, followed by Wood and Wilmink, for all genotypes. Since the CCC value was considered the most informative fit statistics from all the four fit statistics values, the Nelder model was chosen as the best model according to the CCC value. The predicted milk yields using the Rook and Sikka models were significantly higher than all other models for all the genotypes. In general, empirical models were more effective in describing the lactation curve than mechanistic models.

(**Key words:** Lactation curves, Mathematical models, Predicted milk yield, Model fitness)

Abbreviation key: AIC = Akaike information criteria, R^2 = Coefficient of determination, RootMSPE = Root mean square prediction error, CCC = Concordance correlation coefficient.

4.2 Introduction

The Bangladesh Milk Producer's Cooperative Union Limited (BMPCUL), has around 40,000 small-holder dairy farmers, who are members of about 345 primary dairy cooperatives. They milk mostly Pabna cattle, which were developed through the natural mating of local cows with Hariana, Red-Sindhi and Multani (Sahiwal) bulls. Hermans et al. (1989) and Udo et al. (1990) monitored cattle performance in the greater Pabna district and they identified two cattle production systems: a draught–oriented system with local Deshi cattle, and the more milk-oriented production system using the Pabna milking cow (PMC). The PMC is regularly crossed with Sahiwal, Holstein-Friesian and Jersey breeds.

In Bangladesh, there is no well-developed recording system for dairy cattle genetic evaluation and improvement. However, Non-Government Organizations (NGO's), private farms and companies maintain milk and health records. The Bangladesh Agricultural University (BAU), Bangladesh Livestock Research Institute (BLRI) and BMPCUL also maintain milk, pedigree and health records of their herds. In the BMPCUL milk-shed area not all cows are properly tagged, and also, management and rearing conditions are difficult, and vary throughout the year. During the wet season all dairy cattle are kept in unplanned semi-intensive housing, where they are fed mainly paddy straw. In the dry season animals are grazed on pasture land, popularly known as Bathan. Throughout the year lactating cows are fed 2-3 kg/day/cow of concentrates. For various nutritional experiments, genetic evaluations and other research projects, BMPCUL and BLRI sometimes keep individual cow productive and reproductive performance records of the different breeds and crossbreds, enlisting the help of their research and technical staff.

BMPCUL farmers record the total amount of milk produced by each cow every 30 days. Sometimes it is of interest to estimate the total lactation yield from these monthly records. For example, when conducting feeding trials, estimating genetic merit, economic evaluation of different management schemes, and forecasting herd performance for a known period (Goodall, 1986 and Groenewald et al., 1995). For PMC, milk production continues to increase for about 6-8 weeks after parturition

(Singh, 1973), followed by a gradual decline throughout the remainder of lactation, which lasts about 270 days.

Mathematical models are required to predict the total amount of milk yield throughout the entire milking period, from the regularly recorded daily yields. It is also typical to standardise the number of days in the milking period for all cows. Mathematical models of lactation yields were developed in the 1960s when Wood (1967) proposed the incomplete gamma function. Before Wood, other authors (Gaines, 1927 and Nelder, 1966) predicted lactation with simple mathematical models, which had limited accuracy. Since Wood, various models describing the lactation curve in dairy cows have been reported in the literature (e.g, Schaeffer et al., 1977; Coby and Le Du, 1978; Gaskins and Anderson, 1980; Ali and Schaeffer, 1987; Wilmink, 1987; Rook et al., 1993; Guo and Swalve, 1995; Dijkstra et al., 1997; Pollott, 2000; Ødegard et al., 2003 and Maccciota et al., 2005), but their applicability under tropical conditions has received limited investigation (Val-Arreola et al., 2004). In Bangladesh no such studies have been undertaken. All of the above mentioned models are either simple empirical or more mechanistic. Therefore, as a representation of all the models there were ten models were considered in describing the lactation curves under the current study.

The objectives of this study were to: (i) examine the lactation curve for PMC and its crossbred (F_1) cows under cooperative dairying in Bangladesh (ii) compare a number of mathematical models for predicting lactation curves and (iii) determine the most suitable mathematical models, or set of models, for predicting milk yield under cooperative dairying in Bangladesh.

4.3 Materials and Methods

4.3.1 Data Sources

The detail of the husbandry and management system under cooperative dairying in Bangladesh was described by Udo et al. (1992). Measurements of milk production traits of Pabna cattle, Australian-Friesian-Sahiwal × Pabna, Holstein × Pabna, Jersey × Pabna and Sahiwal × Pabna genotypes were obtained from the Animal Breeding Section of BMPCUL. The data covered the calving years from 1999 to 2001; each year being divided into two calving seasons: dry and wet. Most data was from first lactation cows only. Milk yield data was recorded within 15 days of calving, and collected continuously until the end of lactation at an interval of 30 days for each individual cow. Occasionally, the milk recorder failed to recorded milk data in the desired day due to unavoidable circumstances. Cows with less than four herd test records were edited from the data, leaving 7340 records for analysis. In this study, 9 test day milk yield records on 738 cows were used to predict lactation yields set to 270 days. The lactation milk yield was calculated by the BMPCUL technical and research staff as 15 days times the 15 day milk yield plus 30 days times 45 day milk yield etc. up to the end of lactation. This calculation takes no account of the lactation curve, but nevertheless will give a modestly accurate estimate of the total yield due to the regular recording of the milk yield. From the recorded data, the average lactation milk yield and the lactation length of all the genotypes, was estimated in a completely randomised design (CRD) and the mean differences were compared using the least significant difference (LSD) test (Steel et al., 1997).

The steps undertaken in the following analyses include:

Step1. Lactation yields calculated by the BMPCUL technical and research staff being subjected to an analysis of variance to examine whether there were differences between the breed groups.

Step 2. Ten mathematical models were applied to the 9 test day records of 738 cows in two calving seasons and three calving years. Parameters were obtained for each mathematical model by fitting each test day milk yield for each cow as a dependent variable and test days in milk as independent variables with the PROC MIXED and PROC NLMIXED procedures of SAS (SAS, 2000).

Step 3. A comparison of the recorded milk yield, with the predicted yield, resulted in four fit statistics (AIC, R^2, CCC and RootMSPE).

Step 5. Predicted 270 day lactation milk yields, were estimated by fitting the model parameters with test day yields of each cow.

Step 6. A common statistical model (see below) was used to obtained the least square means (±standard error) and significant differences for each parameter (a, b, c, d and k) estimated from the 10 mathematical models, the predicted 270 day lactation milk yields and for each fit statistics parameter (AIC, R^2, CCC and RootMSPE) in PROC MIXED of SAS.

Step 7. Least squares means ((±standard error) for the model parameters and predicted 270 day milk yield were used to compare the performances of the mathematical models, between the breeds and their crosses. Differences were considered to be significant if $P < 0.05$.

4.3.2 Lactation equations

Ten empirical and mechanistic mathematical models (Table 4.1) were fitted to unadjusted daily milk yields recorded at 30 day intervals throughout lactation.

Ganies: a simple 2-parameter model of exponential decay; this was an early attempt to model the lactation curve by Gaines in 1927 (cited by Thornley and France, 2005). The model takes no account of a rise to peak yield after calving.

Wood: the widely applied gamma equation, which consists of 3 parameters and takes into account the rise to peak lactation, and the decay to drying off (Wood, 1967).

Polynomial: the five degree polynomial can provide a very good fit to data. However an excellent fit of a polynomial model cannot be interpreted as an indication that it is, in fact, the true model (Sit and Poulin-Costello, 1994). It is unbound; that is, as x (days in milk) increases indefinitely, the function, y increases or decreases without limit.

Sikka: exponential functions proposed by Sikka (1950); this model considered the initial rise in the milk yields.

Ali: Ali and Schaeffer (1993) proposed a polynomial regression, where both random regressions and covariance functions were selected to compare the differences in model flexibility, due to the number of parameters and the degree of correlation between them. This is in contrast to simple polynomial regressions which ignore the covariance in test day yields.

Legendre: the Legendre polynomial is similar to the model proposed by Ali and Schaeffer; however, in Legendre polynomials, the orders 3, 4 and 5 were used to model the additive genetic and permanent environmental effects on the animal, and the same polynomials were included in the model as fixed regressions. Functions of P_j of Legendre polynomials were calculated as P_0 (t) = 1, P_1 (t) = t, P_2 (t) =1/2($3t^2$-1), P_3 (t) = 1/2($5t^3$-3t) and P_4 (t) = 1/8($35t^4$-$30t^2$+3) (Brotherstone et al., 2000). As the Legendre polynomials are conventionally defined in the range $-1 \leq t \leq +1$, and are orthogonal within this range, days in milk was standardised to lie between -1 and +1 before evaluating the polynomials.

Wilmink: a combined exponential and linear model was proposed by Wilmink (1987). The parameters of this model can be reduced to a 3-parameter linear model by assuming the k exponent is a suitable fixed value. In the present study, k was assumed to be 0.05, which was estimated in a preliminary analysis as the best fitting value for the mean data.

Nelder: is a derivation of the Sikka model proposed by Nelder (1966) using an inverse exponential parabolic function. Inverse polynomials are generally non-negative, bounded, and have a second-order form which has no built-in symmetry. The inverse polynomial overcomes the objections of ordinary polynomials (Nelder, 1966).

Rook: Rook et al. (1993) represented the lactation curve as a multiplicative mixture of cell growth and death processes (Dijkstra et al., 1997 and Thornley and France, 2005).

Dijkstra: derived from mechanistic models of the mammary gland by Dijkstra et al. (1997). The Dijkstra model is based on a set of differential equations representing cell proliferation and cell death in the mammary gland (Diskstra et al., 1997 and Thornley and France, 2005) and yield a 4-parameter equation.

Table 4.1: Mathematical equations used to describe the lactation curve of dairy cows

Author	Equation[1]
Gaines (1927)	$Y = ae^{-bt}$
Wood (1967)	$Y = at^{b}e^{-ct}$
Polynomial	$Y = a + bt + ct^2 + dt^3 + kt^4$
Sikka (1950)	$Y = ae^{(bt+ct^2)}$
Ali and Schaeffer (1987)	$Y = a + b(t/270) + c(t/270)^2 + d\log(270/t) + k\log(270/t)^2$
Legendre Polynomials	$Y = aP_0 + bP_1 + cP_2 + dP_3 + kP_4$
Wilmink (1987)	$Y = a + bt + ce^{-kt}$
Nelder* (1966)	$\frac{t}{Y} = a + bt + ct^2 + dt^3$
Rook et al. (1993)	$Y = a\{1/[1 + b/(c + t)]\}e^{-dt}$
Dijkstra et al. (1997)	$Y = ae[b(1 - e^{-ct})/c - dt]$

[1] Y is milk yield (kg/d), t is time of lactation (days in milk), and a, b, c, d and k are parameters that define the scale and shape of the curve. It should be noted that the same symbol in different equations may represent a different component of the lactation curves (see Table 4.2).

*In the original paper of Nelder (1966) the model was presented as cubic term, however in this study with the addition of a parameter (d) a modified Nelder model was studied.

For the equations given in Table 4.1 parameter a is always the y-intercept; it controls the vertical position of the curves when plotting daily milk yield against days in lactation. Generally, parameters b and c control the height of the maximum yield and parameters d and k shift the curve up or down to the y-axis. The parameters a, b, c, d and k work together with days in milk, to make the shape and placement/position of each curve. The effects of the parameters on curve shape are presented in Table 4.2.

4.3.3 Statistical analysis

The exponential decay (Gaines model) and gamma-type (Wood model) functions were transformed to linear forms to enable the estimation of the unknown parameters using PROC GLM of SAS (SAS, 2000). The fifth-order polynomial, Legendre polynomial and Ali and Schaeffer polynomial regression, were fitted using PROC GLM of SAS to estimate their parameters. All other models were fitted using PROC NLIN of SAS to estimate their parameters.

The goodness of fit of predicted values to actual test day records was indicated by a number of model statistics: the Akaike Information Criteria (AIC); Coefficient of Determination (R^2); Concordance Correlation Coefficient (CCC) and Root Mean Square Prediction Error (RootMSPE). The AIC combine the maximum likelihood (data- fitting) and the choice of model, by penalising the (log) maximum likelihood with a term related to model complexity (Val-Arreola et al., 2004). Smaller values of AIC indicate a better fit when comparing the models. An assessment of the error of predicted values relative to observed values was made by the calculation of RootMSPE. The three values (AIC, R^2 and RootMSPE) were obtained by fitting each predicted test day milk yield for each cow from each mathematical model, as a dependent variable with model parameters (a, b, c, d and k) and test days in milk as independent variables with the PROC MIXED and PROC NLMIXED procedures of SAS (SAS, 2000).

The CCC is an omnibus statistic used to test simultaneously and jointly for accuracy and precision of the models (Runze and Chow, 2005) and CCC assess the systematic error of actual and predicted values (Pierre, 2005). The CCC (Lin, 1989) was calculated as:

$$\text{CCC} = \frac{2S_{AP}}{S_A^2 + S_P^2 + (\overline{A} - \overline{P})^2}$$

where, $\overline{A} = \frac{1}{n}\sum_{i=1}^{n} A_i$, $\overline{P} = \frac{1}{n}\sum_{i=1}^{n} P_i$, $S_A^2 = \frac{1}{n}\sum_{i=1}^{n}(A_i - \overline{A})^2$, $S_P^2 = \frac{1}{n}\sum_{i=1}^{n}(P_i - \overline{P})^2$,

$$s_{AP} = \frac{1}{n}\sum_{i=1}^{n}(A_i - \overline{A})(P_i - \overline{P}),\ s_A = \sqrt{s_A^2},$$

A_i is the actual milk yield at day i and P_i is the predicted milk yield at day i.

After fitting the above models a set of parameters (a, b, c, d, and k) and goodness of fit values (AIC, R^2, CCC and RootMSPE) were available for each of the 738 cows for each mathematical model.

Table 4.2: Effects of parameters on curve shapes

Equations	Parameters			
	b	c	d	k
Ganies	Curve shape			
Wood	Curve height	Parabola up or down on y axis		
Polynomial	Curve shape	Parabola up or down on y axis	Curve shape	Parabola up or down on y axis
Sikka	Curve height	Parabola up or down on y axis		
Ali	Parabola up or down on y axis	Curve height	Curve shape	Curve shape
Legendre	Curve shape	Parabola up or down on y axis	Curve shape	Curve shape
Wilmink	Parabola up or down on y axis	Curve shape		
Nelder	Curve shape	Parabola up or down on y axis	Parabola up or down on y axis	
Rook	Curve height	Curve shape	Parabola up or down on y axis	
Diskstra	Curve height	Curve shape	Parabola up or down on y axis	

The predicted 270 day lactation yield for each cow from each mathematical model was obtained by including its set of parameter values in PROC GLM of SAS for the Gaines, Polynomial, Legendre polynomial and Ali polynomial regression models and PROC NLIN of SAS for all other models.

The following statistical model was used to obtain the least square means (±standard error) for each parameter (a, b, c, d and k) estimating from the 10 mathematical models, the predicted 270 day lactation milk yields and for each fit statistic parameter (AIC, R^2, CCC and RootMSPE).

$$Y_{ijkl} = \mu + \beta_i + \gamma_j + S_k + \beta\gamma_{ij} + \beta S_{ik} + e_{ijkl}$$

Where Y_{ijkl} represents the parameter (predicted milk yield, a, b, c, d, k and fit statistics);

μ is the overall mean;

β_i is the effect of the i^th^ genotype;

γ_j is the effect of j^th^ year of calving;

S_k is the effect of k^th^ calving season;

$\beta\gamma_{ij}$ is the effect of interaction between the i^{th} genotype and the j^{th} year of calving;

βS_{ik} is the effect of interaction between the i^{th} genotype and the k^{th} calving season;

e_{ijkl} is the random residual effect distributed as $N(0, \sigma^2)$.

The interaction of the year and calving season was found to be non-significant and so was not fitted in the model.

Least square means (±standard error) for the model parameters, and the predicted 270 day milk yield were used to compare the performance of the mathematical models between breeds and their crosses. To assist with the comparison of the predicted 270 day milk yields, the least square means (LSM) for Pabna cattle in the case of breed, and the LSM for the Wood model in the case of the mathematical model were considered the standards, and set to 100, with all other breeds and models being ranked relative to Pabna cattle or to the Wood model, respectively. In order to select the best model(s) for each breed(s) the fit statistic (AIC, R^2, CCC and RootMSPE) values were used.

4.4 Results

4.4.1 Lactation milk yield and lactation curves of different breeds

The number of cows, total lactation milk yield estimated by BMPCUL staff and lactation length of different genotypes are shown in Table 4.3. Australian-Friesian-Sahiwal × Pabna and Holstein × Pabna genotypes have the highest lactation yield and lactation length. Figure 4.1 shows the lactation curves of the five genotypes based on the raw data. Peak milk yield was obtained in all genotypes at about 75 days in milk (DIM), followed by a gradual decline. Figure 4.1 suggests that the different genotypes might have different lactation curve shapes.

Table 4.3: The number of cows, lactation yield and lactation length of different breed groups as calculated by BMPCUL staff

Breed group	No of cows	Lactation milk yield, kg (Mean ± SE)	Lactation length, days (Mean ±SE)
P	185	1503^{y} ± 31.15	268.63^{y} ± 3.10
A × P	53	1632^{x} ± 62.09	282.80^{x} ± 5.28
H × P	242	1619^{x} ± 28.84	280.35^{xy} ± 2.61
J × P	31	1517^{y} ± 65.39	267.48^{y} ± 2.61
S × P	207	1548^{xy} ± 24.89	271.30^{y}± 6.84

Legends: P = Pabna Cattle, A = Australian-Friesian-Sahiwal H = Holstein, S = Sahiwal and J = Jersey.

Means with different superscripts are different at P < 5%.

4.4.2 Effects of genotypes

The comparisons of ten mathematical models for five different genotypes were carried out according to the shape of the curve, model performance, and model parameters.

4.4.2.1 Shape of the lactation curves

Figures 4.2 and 4.3 show the fit of each mathematical model to the test day data, with days in milk (DIM) for each of the Pabna and Holstein × Pabna genotypes, and with figures for the other 3 genotypes being shown in Appendix 2(B). The results indicate that different models can be fitted to the data with varying degrees of accuracy using linear and non-linear regression models (see below).

Figures 4.2, 4.3 and Appendix 2(B) show that the Gaines, Rook and Diskstra models poorly represent the data. These figures suggested that the predicted peak yield occurred at parturition for all genotypes for the Ganies and Rook models. Ali polynomial regression model gave a peak at 15 DIM for all the genotypes. The predicted peak yield for all the genotypes in the remaining mathematical models was similar, ranging from 43 DIM (Jersey × Pabna) to 45 DIM (Pabna, Australian-Friesian-Sahiwal × Pabna and Sahiwal × Pabna) except for the Legendre polynomials, Polynomial and Nelder models. The Legendre polynomials and Polynomial models showed peak lactation occurred at 45 DIM for all genotypes except the Holstein × Pabna and Jersey × Pabna, where the predicted peak occurred at 75 DIM and 73 DIM, respectively. The Nelder model gave a peak at 45 DIM for all genotypes except for the Australian-Friesian-Sahiwal × Pabna and Jersey × Pabna genotypes which peaked at 15 DIM and 73 DIM, respectively.

4.4.2.2 Model performance

For the model performance study, the four different fit statistics (AIC, R^2, CCC and RootMSPE) with their standard errors are presented in Table 4.4. The Rook and Dijkstra models were not considered further due to their unsuitable model parameters and poor fit statistics values. The Gaines model was also excluded from further consideration, as it did not allow for the shape of the lactation curve. From Table 4.4, within the model between breeds, each of the fit statistics were fairly consistent, except for the RootMSPE of the Sikka model for Pabna cattle.

The AIC values for the Ali (10.31 to 11.50), Sikka (20.34 to 23.28) and Wilmink (23.92 to 25.94) models were lower than the other models in all genotypes, which indicated a good fit of the models to the data. There were no significant differences found between breeds for AIC of these three models. The AIC values for Legendre polynomials were very high, indicating poor fitting to the raw data. The AIC values for all the remaining models were intermediate and indicated their moderate fit.

The R^2 values indicated that the Legendre polynomials (0.94-0.96) and Ali polynomial regression (0.85 to 93) gave the best fits for all genotypes. There were no significant differences found between genotypes for R^2 values of Legendre polynomials, but in the case of Ali polynomial regression the Australian-Friesian-Sahiwal × Pabna, Holstein × Pabna and Sahiwal × Pabna genotypes showed significantly higher R^2 values than other genotypes. The R^2 values for Nelder, Sikka and Wilmink models showed moderate fits to all breed groups.

The RootMSPE for the Nelder (0.17-0.20) and Wood (0.21-0.23) models indicated a good fit for all genotypes. The RootMSPE value of Nelder model fitted better to the Australian-Friesian-Sahiwal × Pabna and Holstein × Pabna genotypes compared with other genotypes.

CCC values indicated the Nelder, Wood, Polynomial, Wilmink and Sikka models were good fits for all genotypes. The CCC values for the Australian-Friesian-Sahiwal × Pabna in the Polynomial model and the Jersey × Pabna for the Wilmink and Nelder models were significantly higher than the all other genotypes indicating their better fit for these breeds.

4.4.2.3 Model parameters

The estimated parameters (a, b, c, d and k) for the 10 mathematical models and predicted 270 days milk yields are presented in Table 4.5. The model parameters were compared within model between breeds. The parameters of Rook and Diskstra models were not evaluated due to the poor fitting of the predicted lactation curves to the raw data. The Ganies is a very simple, two parametric model, which did not allow for the shape of the lactation curve and was not further evaluated. However, the parameters and the predicted lactation milk yield value of these models were presented in Table 4.5 for information only.

4.4.2.4 Predicted lactation milk yields

The predicted lactation milk yields are presented in Table 4.5. The Pabna cattle in the case of breeds and the Wood model in the case of models were considered as standards and set at 100 (Table 4.6).

When considering the mathematical models, the highest predicted lactation milk yield was obtained for Pabna cattle, Holstein × Pabna, Jersey × Pabna and Sahiwal × Pabna by fitting the parameters of the Rook model, which was about 20% higher, when compared with the Wood model. The lowest yield was obtained after fitting the parameters of the Ali polynomial regression. All other models produced predicted lactation milk yields similar to the Wood model.

The predicted lactation milk yield of Australian-Friesian-Sahiwal × Pabna and Holstein × Pabna genotypes were more than 20% higher compared with all other genotypes in all the models except for Wood and Polynomial models. Predicted lactation milk yield of other genotypes were similar to Pabna cattle for all the models.

4.4.3 Effects of years and seasons

The effects of calving years (1999 to 2001), seasons (dry and wet) and their interactions with different genotypes on the parameters for ten different mathematical models, goodness of fit statistics and the predicted lactation milk yields are given in Appendix 2 (A).

4.4.3.1 Model performance

The effects of calving years (1999 to 2001), seasons (dry and wet) and their interactions with different genotypes were evaluated by four goodness of fit statistics. Only the values of RootMSPE for the Nelder and Wilmink models were significantly different between years, and 2001 showed higher than other year in the case of the Nelder model. The other three fit statistics did not show significant differences between years.

The values of RootMSPE for the Nelder model were significantly higher in dry than wet seasons. All four fit statistics for the Wilmink, Wood, Polynomial, Sikka, Rook and Legendre polynomials models showed no significant differences between seasons.

4.4.3.2 Model parameters

The curve shape for Polynomial and Gaines models, curve height for the Dijkastra, and Rook models and position of the parabola for the Ali polynomial regression and Wilmink models were significantly different between years. For all other parameters of the models there were no significant differences found between years.

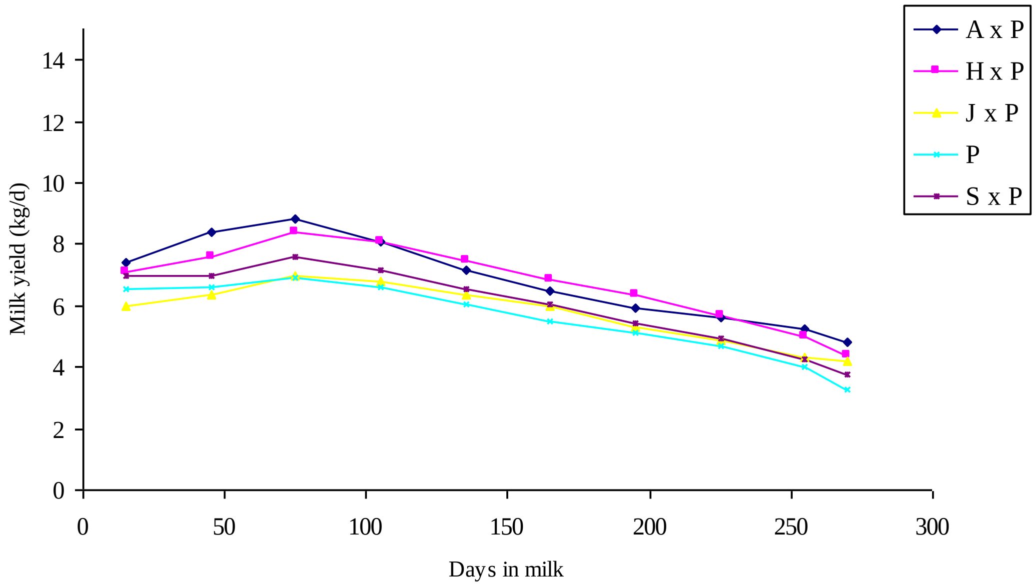
For the mathematical models, no significant differences were found between seasons for the model parameters except for the Nelder model. The parameters of the Polynomial, Legendre polynomials, Dijkastra and Rook models were not significantly different between seasons and breeds.

4.4.3.3 Predicted lactation milk yield

The predicted lactation milk yields were significantly different between years (8 to18%) for the Wood, Gaines and Ali polynomial regression models. The predicted lactation milk yield of Jersey × Pabna was significantly different between years (20 to 28%) for all models except the Gaines model and Legendre polynomials and for Pabna cattle. Differences were found for Ali and Sikka models between the year 1999 and 2000, respectively. There were no significant differences found for predicted lactation milk yields between years within a genotype for all the models for Sahiwal × Pabna and Holstein × Pabna, except the Gaines model between 1999 and 2001.

The predicted lactation milk yields were significantly different between seasons for the Gaines and Sikka models, but in all other models, no differences were found. The predicted lactation milk yields of Australian-Friesian-Sahiwal × Pabna, Holstein × Pabna in both seasons and for Sahiwal × Pabna in the wet season were significantly higher than Jersey × Pabna and Pabna cattle for all models.

Figure 4.1: Lactation curve of different genotypes of cow under cooperative dairying in Bangladesh



Legends: A × P = Australian-Friesian-Sahiwal × Pabna, H × P = Holstein × Pabna, J × P = Jersey × Pabna, P = Pabna cattle and S × P = Sahiwal × Pabna

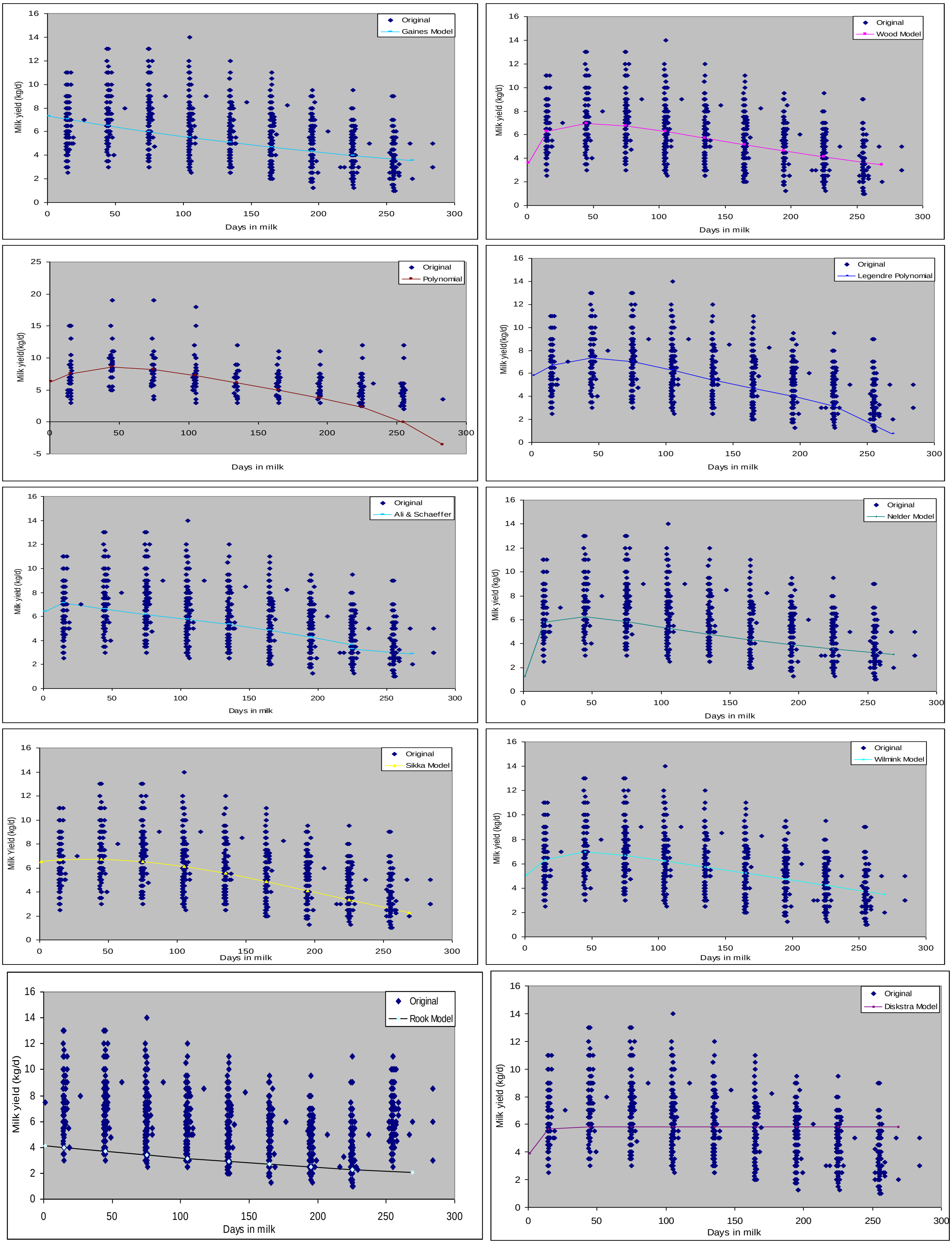


Figure 4.2: Lactation curves for Pabna cows. Lines were obtained by fitting the candidate functions: Gaines, Wood, Polynomials, Legendre Polynomials, Ali polynomial regression, Nelder, Sikka, Wilmink, Rook and Dijkstra equations

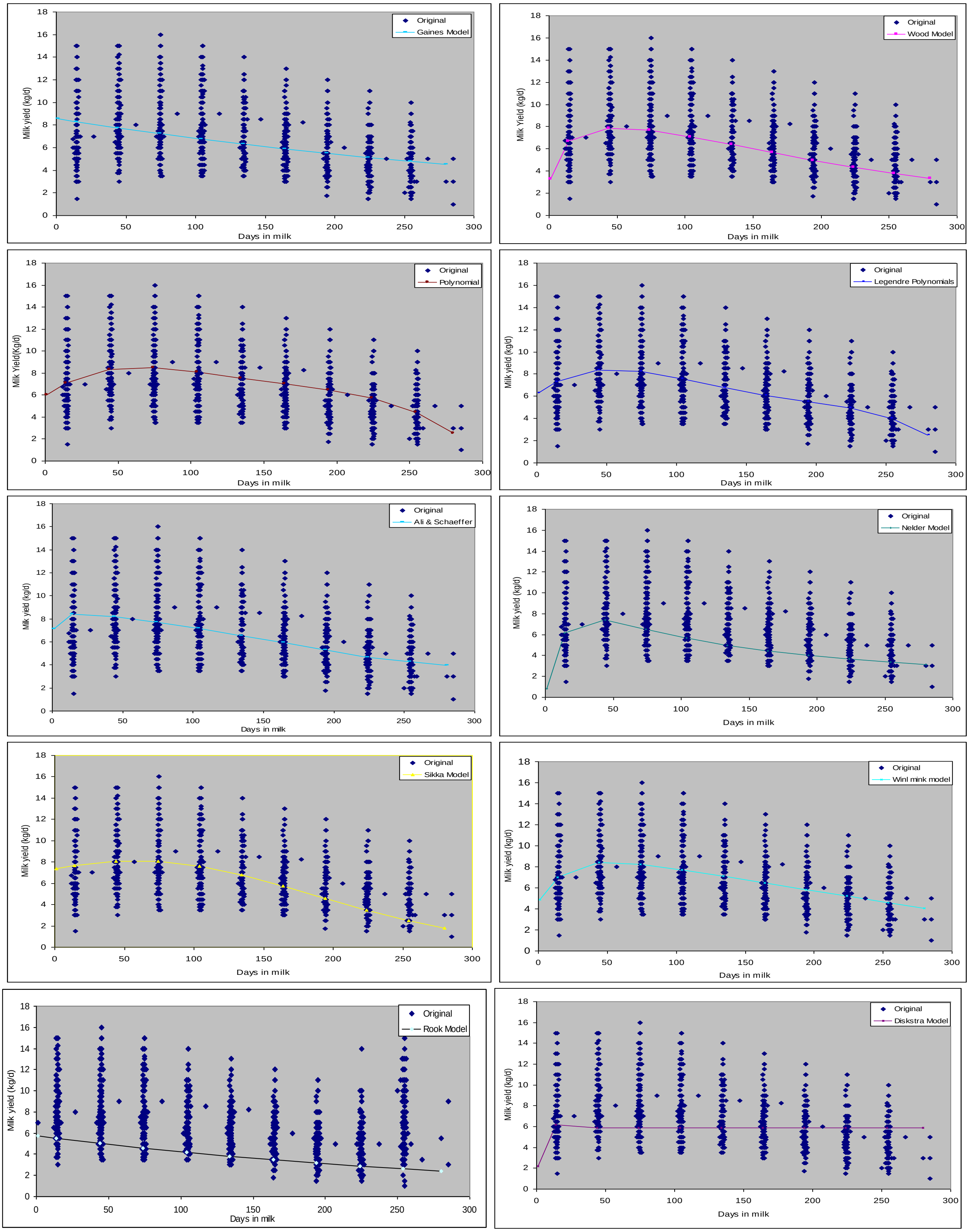


Figure 4.3: Lactation curves for Holstein × Pabna cows. Lines were obtained by fitting the candidate functions: Gaines, Wood, Polynomials Legendre Polynomials, Ali and Schaeffer polynomial regression, Nelder, Sikka, Wilmink, Rook and Dijkstra equations

Table 4.4: Comparison of model performance using different fit statistics (±standard error)

Breed group	Item	Equations						
		Wood	Polynomial	Ali	Legendre polynomial	Nelder	Sikka	Wilmink
P	AIC	67.03 ± 0.74	41.59 ± 0.68	11.50 ± 0.49	116.40^{x} ± 1.83	65.44^{xy} ± 0.75	22.43 ± 1.40	25.94 ± 0.71
	R^2	0.53^{x} ± 0.02	0.55^{x} ± 0.02	0.89^{y} ± 0.011	0.95 ± 0.004	0.74^{y} ± 0.016	0.71 ± 0.02	0.78^{x} ± 0.017
	RootMSPE	0.24^{xy} ± 0.08	0.63^{x} ± 0.09	0.55 ± 0.03	1.30 ± 0.06	0.20^{y} ± 0.05	1.2^{y} ± 0.52	0.70^{y} ± 0.22
	CCC	0.87 ± 0.01	0.87^{y} ± 0.01	0.12^{x} ± 0.02	0.70^{x} ± 0.02	0.88^{y} ± 0.025	0.82 ± 0.017	0.86^{y} ± 0.14
A×P	AIC	68.05 ± 1.26	42.36 ± 1.16	10.31 ± 0.85	125.19^{y} ± 3.12	69.53^{y} ± 1.27	21.69 ± 2.38	23.92 ± 1.20
	R^2	0.55^{x} ± 0.04	0.57^{x} ± 0.04	0.93^{x} ± 0.018	0.95 ± 0.007	0.78^{x} ± 0.03	0.67 ± 0.03	0.73^{y} ± 0.03
	RootMSPE	0.23^{x} ± 0.01	0.58^{x} ± 0.15	0.54 ± 0.05	1.45 ± 0.11	0.17^{x} ± 0.06	0.79^{x} ± 0.68	0.62^{y} ± 0.30
	CCC	0.89 ± 0.02	0.91^{x} ± 0.02	0.03^{y} ± 0.04	0.65^{y} ± 0.03	0.88^{y} ± 0.03	0.77 ± 0.03	0.84^{y} ± 0.24
H ×P	AIC	68.16 ± 0.62	42.19 ± 0.57	11.54 ± 0.42	119.12^{x} ± 1.54	69.24^{y} ± 0.63	23.28 ± 1.18	25.31 ± 0.59
	R^2	0.57^{x} ± 0.02	0.61^{x} ± 0.02	0.92^{x} ± 0.009	0.96 ± 0.003	0.80^{x} ± 0.013	0.73 ± 0.017	0.81^{x} ± 0.01
	RootMSPE	0.21^{x} ± 0.07	0.66^{y} ± 0.08	0.54 ± 0.022	1.31 ± 0.05	0.17^{x} ± 0.04	0.80^{x} ± 0.48	0.62^{y} ± 0.20
	CCC	0.88 ± 0.009	0.86^{y} ± 0.02	0.11^{x} ± 0.02	0.67^{xy} ± 0.01	0.89^{y} ± 0.01	0.80 ± 0.015	0.84^{y} ± 0.12
J×P	AIC	67.51 ± 1.63	40.01 ± 1.50	11.27 ± 1.10	120.68^{x} ± 4.04	62.07^{x} ± 1.65	20.34 ± 3.09	24.17 ± 1.56
	R^2	0.43^{y} ± 0.05	0.49^{y} ± 0.05	0.85^{y} ± 0.023	0.94 ± 0.009	0.69^{y} ± 0.03	0.74 ± 0.04	0.78^{x} ± 0.04
	RootMSPE	0.28^{y} ± 0.02	0.59^{x} ± 0.19	0.55 ± 0.06	1.51 ± 0.18	0.20^{y} ± 0.07	0.82^{x} ± 0.77	0.54^{x} ± 0.33
	CCC	0.87 ± 0.02	0.86^{y} ± 0.02	0.16^{x} ± 0.05	0.66^{y} ± 0.03	0.94^{x} ± 0.03	0.78 ± 0.04	0.90^{x} ± 0.31
S×P	AIC	68.06 ± 0.62	41.41 ± 0.57	10.68 ± 0.42	117.65^{x} ± 1.54	67.14^{y} ± 0.63	21.56 ± 1.18	25.50 ± 0.59
	R^2	0.58^{x} ± 0.02	0.61^{x} ± 0.02	0.91^{x} ± 0.009	0.96 ± 0.003	0.75^{xy} ± 0.01	0.72 ± 0.017	0.79^{x} ± 0.014
	RootMSPE	0.21^{x} ± 0.06	0.66^{y} ± 0.08	0.53 ± 0.022	1.18 ± 0.05	0.18^{xy} ± 0.04	0.87^{x} ± 0.69	0.65^{y} ± 0.20
	CCC	0.89 ± 0.009	0.86^{y} ± 0.01	0.11^{x} ± 0.02	0.68^{x} ± 0.01	0.90^{xy} ± 0.01	0.79 ± 0.015	0.85^{y} ± 0.12

Legends: A= Australian-Sahiwal-Friesian, H=Holstein, J=Jersey, P=Pabna cattle, S=Sahiwal, AIC=Akaike Information Criteria, R^2= RSquare, RootMSE=Root mean square prediction error, and CCC= Concordance Correlation Coefficient. Means with different superscripts are different at P<5%.

The significance test was showed in between breeds within the model.

Table 4.5: Parameter estimates and other measures when models were fitted to the different breed groups under cooperative dairying in Bangladesh (±standard error)

Breed group	Item	Equations									
		Gaines	Wood	Polynomial	Legendre polynomial	Ali	Nelder	Sikka	Wilmink	Rook	Dijkstra
P	a	1.99^{y}±0.03	1.29^{x} ± 0.06	5.62±0.17	5.75±0.27	-10.16±6.06	0.68^{y}±0.37	6.54^{y}±0.23	8.05^{y}±0.25	5.54 ±16.28	5.44±0.32
	b	-0.0027^{y}±0.0001	0.23^{y}±0.01	0.075^{y}±0.01	0.079±0.009	22.25±9.15	0.12^{x}±0.03	0.0015^{y}±0.0005	-0.017±0.001	-3301.42±52164	0.068±0.017
	c		-0.005±0.0002	-0.0011^{y}±0.00001	-0.0008^{xy}±0.00009	-8.81±3.28	0.00048^{y}±0.0018	-0.00002±4.237E-6	-3.08^{x}±0.38	-10033±22364	0.18±0.062
	d			5.026E-6^{y}	2.304E-6	11.61±3.68	7.892E-7^{y}±5.003E-6			0.0026±0.0004	0.037±0.009
	k			-8.55E-9^{y}	-2.25E-9	-2.18±0.61					
	plmy	1482.86^{y}±42.23	1574.09^{y}±46.38	1553.79^{y}±41.60	1798.32^{y}±44.65	859.54^{y}±91.91	1697.42^{y}±34.85	1780.86^{y}±66.84	1698.43^{y}±66.56	1819.25^{y}±69.67	1623.72^{y}± 61.32
A×P	a	2.18^{x}±0.05	1.41^{x}±0.10	6.16±0.31	5.88±0.46	-14.92 ±10.32	3.13^{x}±0.63	8.34^{x}± 0.39	10.02^{x}±0.43	7.89 ±12.22	5.16±0.54
	b	-0.0025^{y}±0.0003	0.23^{y}±0.03	0.111^{x}±0.01	0.122±0.015	27.60±15.57	-0.144^{y}±0.06	0.0015^{y}±0.0008	-0.022±0.0016	2121.12±39164	0.095±0.028
	c		-0.005±0.00033	-0.0016^{xy}±0.0002	-0.0012^{y}±0.0002	-8.06±5.58	0.0058^{x}±0.0014	-0.00002±7.214E-6	-3.85^{x}±0.64	56248±46017	0.0904±0.10
	d			7.659E-6^{x}	3.455E-6	16.88±6.26	-0.00003^{x}±8.52E-6			0.0026±0.0003	0.0059±0.016
	k			-1.28E-8^{y}	-3.26E-9	-3.29±1.04					
	plmy	1876.09^{x}±79.73	1806.25^{x}±78.9	1770.54^{x}±34.78	2174.77^{x}±83.07	1303.66^{x}±85.42	2187.81^{x}±56.49	2368.60^{x}±73.80	2209.69^{x}±63	2299.66^{x}±68.6	2053.79^{x}± 84
H×P	a	2.15^{x}±0.02	1.19^{xy}±0.05	5.94±0.13	6.18±0.23	6.62±5.11	1.15^{x}±0.31	7.37 ^{xy}±0.19	9.92^{x}±0.21	21.34 ±5.93	5.31±0.27
	b	-0.0023^{y}±0.0001	0.30^{x}±0.01	0.097^{x}±0.01	0.098±0.008	-1.27^{y}±7.71	0.067^{x}±0.03	0.0034^{x} ±0.0004	-0.021±0.001	-6856.98±19006	0.098±0.014
	c		-0.006±0.0002	-0.0012^{x}±0.0001	-0.0009^{xy}±0.00007	-1.048±2.76	0.00098^{y}±0.0007	-0.00003±3.572E-6	-5.28^{y}±0.32	-2537.35±22332	0.12±0.052
	d			5.45E-6^{x}	2.484E-6	2.65±3.10	-3.46E-7^{y}±4.215E-6			0.0028±0.0002	0.032±0.0078
	k			-9.13E-9^{x}	-2.29E-9	-0.85±0.51					
	plmy	1869.52^{x}±34.99	1828.10^{x}±39.1	1777.84^{x}±34.78	2048.80^{x}±36.84	1112.54^{x}±240.50	1993.15^{x}±40.49	2135.80^{x}±56.35	1987.06^{x}±56	2183.54^{x}±58.74	1941.90^{x}±51.69

Table 4.5: Continuation-----------------.

Breed group	Item	Equations									
		Ganies	Wood	Polynomial	Legendre polynomial	Ali	Nelder	Sikka	Wilmink	Rook	Diskstra
J×P	a	1.91^{y} ±0.06	1.10^{y}±0.13	5.55±0.41	5.74±0.59	12.32±13.39	0.75^{y}±0.81	5.95^{y}±0.51	8.23^{y}±0.56	12.38±6.96	4.41±0.70
	b	-0.0023^{y}±0.0004	0.28^{xy}±0.04	0.079^{y}±0.02	0.077±0.02	-10.94±20.19	0.165^{x}±0.08	0.0045^{x}±0.0011	-0.017±0.001	-10054±22319	0.078±0.037
	c		-0.0054±0.0004	-0.001^{x}±0.0002	-0.0007^{x}±0.00019	2.61±7.24	-0.00043^{y}±0.002	-0.00003±9.356E-6	-4.55^{y}±0.83	248382±61291	0.056±0.14
	d			4.421E-6^{y}	2.039E-6	-2.10±8.12	4.26E-6^{y}±0.00001			0.0021±0.00018	0.046±0.02
	k			-7.3E-9^{x}	-2E-9	-0.032±1.34					
	plmy	1507.13^{y}±65.36	1599.89^{y}±72.43	1552.47^{y}±90.88	1801.92^{y}±61.01	1152.38^{x}±68.91	1634.85^{y}±45.50	1722.79^{y}±47.60	1622.88^{y}±46.9	1820.12^{y}±53.86	1548.87^{y} ± 35.4
S×P	a	2.09^{y}±0.02	1.18^{y}±0.05	5.75±0.13	5.83±0.23	-2.94±5.12	1.12^{x}±0.31	7.02^{xy}±0.19	9.17^{xy}±0.21	20.52 ±5.94	5.02±0.27
	b	-0.0025^{y}±0.0001	0.28^{xy}±0.01	0.083^{y}±0.01	0.081±0.008	12.93±7.72	0.074^{x}±0.02	0.003^{y}±0.00041	-0.020±0.001	-21409±19034	0.087±0.014
	c		-0.0055±0.0002	-0.0011^{x}±0.0001	-0.0008^{xy}±0.00007	-6.82±2.77	0.00099^{y}±0.0007	-0.00003±3.576E-6	-4.34^{y}±0.32	-7707±22364	0.12±0.052
	d			4.913E-6^{y}	2.167E-6	7.82± 3.10	-3.56E-7^{y}±4.222E-6			0.0025±0.00015	0.025±0.0078
	k			-7.81E-9^{x}	-2.07E-9	-1.62±0.51					
	plmy	1623.94^{y}±32.42	1624.07^{y}±39.15	1622.16^{y}±35.18	1841.29^{y} ± 34.17	859.54^{y} ± 91.91	1822.92^{xy}±34.95	1923.86^{y}±56.41	1818.36^{xy}±56.2	1973.96^{y}±58.80	1742.48^{xy}±51.75

Legends: A= Australian-Friesian-Sahiwal, H=Holstein, J=Jersey, P=Pabna Cattle, S=Sahiwal, a, b, c, d and k are parameters that define the scale and shape of the curve

Plmy = Predicted lactation milk yield, Means with different superscripts are different at $P < 5\%$.

. The significance test was showed in between breeds within the model.

Table 4.6: Comparisons of the predicted lactation milk yield of the different breed groups by using ten different lactation models

Breed group	Equations																			
	Gaines		Wood		Polynomial		Legendre polynomial		Ali		Nelder		Sikka		Wilmink		Rook		Dijkstra	
	BC	MC	BC	MC	BC	MC	BC	MC	BC	MC	BC	MC	BC	MC	BC	MC	BC	MC	BC	MC
P	100	94	100	100	100	99	100	114	100	55	100	108	100	113	100	108	100	116	100	103
A×P	127	104	115	100	114	94	121	120	152	72	129	121	133	131	130	122	126	127	126	114
H ×P	126	102	116	100	104	89	114	112	134	63	117	109	120	117	117	109	120	119	120	106
J×P	102	94	102	100	97	94	100	113	89	48	96	102	97	108	96	101	100	114	95	97
S×P	110	100	103	100	100	96	102	113	100	53	107	112	108	118	107	112	109	122	107	107

Legends: A= Australian- Friesian-Sahiwal, H=Holstein, J=Jersey, P=Pabna Cattle, S=Sahiwal

BC = Breed comparison (P= 100) and MC = Model comparison (Wood =100).

4.5. Discussion

4.5.1 Lactation milk yield of different breeds

According to the simple calculation for lactation yields by BMPCUL technicians the Australian-Friesian-Sahiwal × Pabna and Holstein × Pabna genotypes produced higher lactation yields and had longer lactation lengths than other genotypes (Table 4.3). Similar findings were reported by Hossain (2006); Bhuiyan et al. (1998) and Khan and Khatun (1998). Furthermore, many findings (e.g. Cunningham and Syrstad, 1987; Syrstad, 1989 and Madalena et al., 1990) from other tropical countries have also shown that the first cross of temperate breeds with tropical breeds produce more milk in a tropical environment.

The total lactation milk yields calculated by the BMPCUL technicians (Table 4.3) were lower than the lactation milk yields predicted from the mathematical models (Table 4.5). The primary reasons for the lower yields were that there was no attempt to account for the shape of the lactation curve and there was no adjustment to a common lactation length. The higher milk yields were caused at least in part, by longer lengths of lactation. However, only Pabna and Jersey × Pabna have lactation length less than 270 days. Therefore, when the models adjust the lactation yields to 270 days the other genotypes will be penalised. Generally, the higher lactation lengths have positive effects on the lactation yield was reported by Ruiz et al. (2000) and Tekerli et al. (2000).

The predicted total lactation milk yield (Table 4.5) differed between breeds, mathematical functions of the models and also the predicted ability of the model parameters. Similar factors were reported by Pérochon et al. (1996), Vargas et al. (2000) and Brown et al. (2001) and Koonawootrittriron et al. (2006) for the differences in predicted milk yields from the lactation curve studies.

4.5.2 Models of lactation curves for different genotypes

4.5.2.1 Shape of the lactation curve

Figures 4.2, 4.3 and Appendix 2(B) indicate that the Gaines and Rook models poorly represented the test day records, due to the absence of a predicted lactation peak. Similar results were reported by Val-Arreola et al. (2004) for the Gaines model. The

Dijkstra equation predicted a peak in all genotypes, but its gradual decline did not match the trend shown by the raw data in any of the genotypes. This result is in contrast to those of Dijkstra et al. (1997) and Val-Arreola et al. (2004), who found that the Diskstra equation fitted better than other empirical equations when predicting 305-day lactation yields. This difference in outcome might be attributed to low cow numbers and also to test day records.

The shapes of the predicted lactation curves were similar across all genotypes for the Gaines, Wood, Sikka and Wilmink models. This could be attributed for similar pattern of model parameters appeared of these models for all the genotypes. However, the shape of the lactation curve of the polynomial model was similar for Holstein × Pabna, Jersey × Pabna and Sahiwal × Pabna but different in Pabna cattle and Australian-Friesian-Sahiwal × Pabna. The shape of the lactation curve of Legendre polynomials for Holstein × Pabna and Sahiwal × Pabna were similar, but different for other genotypes. The differences in the shapes of the lactation curves for different genotypes were observed, with the differences of day of peak yield, the steepness and also the flatness of the curves, and these are the results of the differences for predicted model parameters of different models. In addition, the differences of curve shape could be attributed to few test day records prior to the peak, and also to a low number of available records. Similar results were identified by Rekik and Gara (2004), Macciotta et al. (2005) and Silvestre et al. (2006) for the estimation of lactation curve shape. Rekik and Gara (2004) reported that 4% curve shape was varied for each day that the first test-day date delayed.

The differences of the model parameters and the fitness of the fit statistics could be attributed to the differences in model fitting, and also to the effects of genetic groups. The differences of model fitting were reported by Ramirez-Valverde et al. (2003), Val-Arreola et al. (2004), Koonawootrittriron et al. (2006) and Fathi Nasri et al. (2008). The gradual decline in the lactation curve has been reported by Ramirez-Valverde et al. (1998); Tekerli et al. (2000) and Val-Arreola et al. (2004). The most common shape being a rapid increase, followed by a gradual decline until the cow is dried off. The other shape is a gradual decline from parturition. However, several studies (e.g. Ferris et al., 1985; Pérochon et al., 1996; Landete-Castillejos and

Gallego, 2000; Dedkova and Nemcova, 2003; Val-Arreola et al., 2004; Macciotta et al., 2005 and Fathi Nasri et al., 2008), have shown the differences in the general shape of mathematical models, the differences of scaling factors (model parameters) associated with yield at the beginning of lactation, the inclining and declining slopes before and after peak yield, days in milk at peak, and peak and lactation yields of the lactation curves.

4.5.2.2 Model performance

Four fit statistics (AIC, R^2, CCC and RootMSPE) values were used to evaluate the model's performance. Smaller AIC and RootMSPE values indicated a better fit (Motulsky and Christopoulos, 2003 and Val-Arreola et al., 2004) but for R^2 and CCC bigger values indicated superior models (Motulsky and Christopoulos, 2003 and Pierre, 2005). According to the AIC value, the Ali polynomial, Sikka and Wilmink models provided the best fits for Jersey × Pabna and Australian-Friesian-Sahiwal × Pabna genotypes, respectively. The R^2 values of Legendre, Ali polynomial and Wilmink models indicated the best fits for Holstein × Pabna and Sahiwal × Pabna genotypes respectively. A similar finding was observed by Olori et al. (1999) for the Wilmink model. The R^2 value of Nelder and Sikka models was moderate for all the genotypes. However, CCC and RootMSE values indicated that the Nelder model provided the best fit followed by the Wood, Wilmink and Polynomial models, respectively, in all genotypes. All other models showed intermediate fit statistics for CCC and RootMSE values for all the genotypes. Among the four fit statistics, the CCC value was considered the most informative fit statistics, due to it's accuracy and precision and assesability of the systematic error for actual and predicted values (Runze and Chow, 2005 and Pierre, 2005), and therefore these results suggested that Nelder model was the best model. An alternative for choosing the best fitting model would be to derive an index (I) comprising of all four fit statistics value. For example, $I_{Nelder} = W_1 0.74\ (R^2) + W_2 0.20$ (RootMSPE) + $W_3 65.44$ (AIC) + $W_4 0.88$ (CCC), where, W's are index weighting factors, which would be derived based on the variance-covariance relationships between the fit statistics.

Model fitness statistics varied between genotypes and also the differences of the mathematical functions, of the models. The variation of fit of models between breeds may have arisen from the differences in breeds, mathematical functions of the models, differences of test day yield, the amount of data, the number of test day records and the intervals between tests. Differences in lactation curves are a combination of environmental and genetic factors (Pérochon et al., 1996). The effects of the number of test day records and the intervals between tests on the estimation of fit statistics, and also their fitting ability, was reported by Tekerli et al. (2000) and Wiggans et al. (2002).

4.5.3 Effects of years and seasons

The predicted 270-day milk yield was higher in 2001 than in 1999 and 2000 in all the models. The predicted milk yield of Holstein × Pabna cows was significantly higher than all other genotypes, except Pabna cattle within the years. The Sahiwal × Pabna and Holstein × Pabna breeds, showed similar predicted milk yields between the years for all the models, except the Gaines model. Owing to the limited data set, it was not possible to determine whether differences in predicted milk yields between years and within a single year between genotypes, were caused by genetic or environmental factors. Higher predicted milk yields in a particular year might be due to the greater availability of green grasses, good management, or more optimal temperatures, humidity and rainfall. Similarly, the higher production for particular genotypes could be due to breed characteristics, and also the effect of genotype × environment interactions during the year. The differences, of the lactation curves traits can be attributed to both environmental and genetic factors (Rao and Sundaresan, 1979 and Pérochon et al. 1996 and Brown et al. 2001) and they can also be affected by the calving year (Rao and Sundaresan, 1982; Collins and Lueweti, 1991; Tekerli et al., 2000 and Rekik and Gara, 2004).

Predicted milk yields were higher during the dry season than the wet season for all genotypes and all models. The higher yield in the dry season might be attributed to the better feeding, management and favourable weather conditions than those of the wet season. Similar causes for production differences between breeds were reported by Ramirez-Valverde et al. (2003), Val-Arreola et al. (2004), Koonawootrittriron et al. (2006) and Fathi Nasri et al. (2008). Furthermore, the differences in predicted milk yields can be caused by differences in genotypes and environment, as reported by Keown et al. (1986); Rao and Sundaresan (1982); Elston et al. (1989) and Tekerli et al. (2000). Farmers contributing milk to BMPCUL exhibit comparatively better feeding and management of dairy cattle during the dry season, than during the wet season. In the wet season, all breeds and age groups of cattle are kept in unplanned stall feeding conditions where they are fed paddy straw. However, in the dry season cattle are allowed to graze on pasture land, where they are able to consume abundant green grasses. The differences of milk production between seasons, and management systems, were reported by Sherchand et al. (1995), Pérochon et al. (1996) and Val-Arreola et al. (2004).

4.6 Conclusion

The lactation yields calculated by BMPCUL technicians were underestimates of the probable lactation yield for all genotypes, as they failed to account for the shape of lactation curves.

Results of this study indicate that the Nelder model was the most suitable to transform test day milk yields into a 270-day predicted milk yield for all genotypes based on higher CCC and R^2 and lower RootMSPE values. Therefore, the Nelder model will be used in the subsequent chapters of this thesis. The Wood, Wilmink and Polynomial models were the next best models. The Gaines, Rook and Dijkstra equations did not accurately predict the expected shape of the lactation curve and were not considered for further use. All other models were intermediate in their ability to predict lactation curves. The Rook and Sikka models predicted the highest 270-day milk yields for all the genotypes.

There were some limitations in this study: such as the low number of records per genotype representing only three years. Confidence that the correct mathematical model has been chosen would be increased, if additional data were to be collected and added to the current analyses.

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CHAPTER FIVE

Development of a Deterministic Dynamic Model to Estimate Individual Cow and Farm Profit for Dairy Farming under Cooperative Dairying in Bangladesh

5.1 Abstract

The aim of this study was to develop a dairy farm model to estimate the profitability of an individual cow, as well as the whole farm operation under cooperative dairying in Bangladesh. A deterministic, dynamic, model was developed by simulating herd dynamics, nutrition, and the biological and economic performance of an average farm. The energy requirements of calves and cows of different genotypes for maintenance, lactation, pregnancy, body weight gain and cow replacement were estimated. Pabna cattle had the lowest, and Holstein × Pabna the highest Dry Matter requirements. The performance and economic study showed that Holstein crossbreds produced comparatively higher lactation yields as well as profit than other genotypes. The net annual incomes of Pabna cattle, Sahiwal × Pabna, Jersey × Pabna, Australian-Friesian-Sahiwal × Pabna and Holstein × Pabna, were US$115, US$119, US$166, US$209 and US$229, respectively. After considering costs against revenue, the returns on the capital investment in Sahiwal × Pabna, Pabna cattle, Jersey × Pabna, Australian-Freisian-Sahiwal × Pabna and Holstein × Pabna, genotypes were 8.8%, 9.0%, 12.5%, 15.5% and 16.6%, respectively. The outputs of the simulation models were considered to be realistic representations of existing farms. The simulation study showed that dairy farming under cooperative dairying was only modestly profitable. The findings of this study could assist farmers and policy makers in making future farming decisions, and could also assist scientists conducting research under the cooperative dairying system in Bangladesh.

(**Key words:** Farm model, costs, revenues, profit, DM requirements, net return)

5.2. Introduction

Currently, there is a major discrepancy between the level of dairy production and consumer demand in Bangladesh, and the major challenge for the farming community is to produce larger quantities of milk while using sustainable farming practices. However, there exists no well-planned dairy cattle production system in Bangladesh, although the BMPCUL members' dependency on cattle farming is on the increase.

The main aim of farmers in BMPCUL areas is to increase farm profit. Decisions contributing to farm profitability include: the number of cattle to be run; which genotype(s)/ breed(s) are most suitable; what type and level of supplementary feeding is required; the area to be cultivated for fodder; the amount of feed to be conserved to meet periods of feed shortage; and how to breed the cattle effectively.

To aid farmers in making such decisions, the Bangladesh Livestock Research Institute (BLRI) regularly conducts research on genetic evaluation of livestock, as well as undertaking feeding trails in the cooperative areas. However, the results of these studies have not yet been integrated into farm systems, suggesting that additional research efforts are required to estimate maximise benefits for the farmers.

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One way to better understand a farming system is to build a simulation model. Modelling integrates knowledge of the components of a farm system with their interactions and can be used to identify differences in efficiency of production by varying inputs and outputs (Kirk et al., 1988). This assists researchers, policy makers and farmers in making decisions that will improve sustainability and also farm profitability. Various types of models have been developed for temperate environments. Examples include models for determining the most profitable feeding strategies for dairy herds (e.g. DAIRYFEED, Kirk and Olney, 1988), management models (Kirk et al., 1988 and Olney and Kirk, 1989) and whole farm models (Marshall et al., 1991 and Bright et al., 2000). It would be useful to develop a model to integrate management, animal improvement and marketing in order to optimise dairy cattle production within a tropical environment such as Bangladesh.

Economic evaluations of crossbreeding strategies have been conducted under temperate conditions (McDowell and McDaniel, 1968; Touchberry, 1992; McAllister et al., 1994 and Lopez-Villalobos et al., 2000). These studies showed that crossbreeding results in sufficient heterosis to provide greater economic returns than the best of existing breeds. On the other hand, there were some economic evaluation studies carried out in the tropics, but in these studies only a small number of farming activities and constraints were considered for the development of models. For example, Ram and Singh (1975), Parmar and Dev (1978) and Kanchan and Tomar (1984) considered only returns from sales of milk and manure, and the costs associated with milk production, in their economic evaluation. In other profit function studies (e.g. Reddy and Basu, 1985; Madalena et al., 1990 and Kahi et al., 2000), they considered returns from sales of calves, and culled cows, in addition to returns from milk sales. From these profitability models it was reported that the Holstein combinations were superior for milk production to other genotypic combinations in tropical environments (Madalena et al., 1990; Gunjal et al., 1997 and Kahi et al., 2000). As in the existing tropical study, it was found that there was some information missing on the development of models, hence in the present models, all the farming components within Bangladeshi conditions were considered.

In this chapter, the following objectives were addressed under cooperative dairying in Bangladesh: i) to develop a dairy farm model for maximised profit, ii) to estimate the profit of individual cows of the Pabna cattle and its crossbreds, iii) to estimate whole farm profit, and iv) to compare five genotypes (Pabna, Australian-Freisian-Sahiwal × Pabna, Holstein × Pabna, Jersey × Pabna and Sahiwal × Pabna) using the farm model.

5.3 General concepts

The general concepts of the model are described below.

- The rearing of young stock is treated separately from other farm activities, because a proportion of heifers are either purchased from either the market or from another farmer's dairy herd.

- It is assumed that fresh and processed feed consumed by the dairy cows is produced on the farm, with some of the concentrate being procured from the market.

- The sale value of draught power and manure was included as revenue.

- The performance, revenue and costs of cows are estimated year-wise and allow for a 20% per year cow replacement rate at regular intervals within the lactation period.

The major components of the model are represented in Figure 5.1.

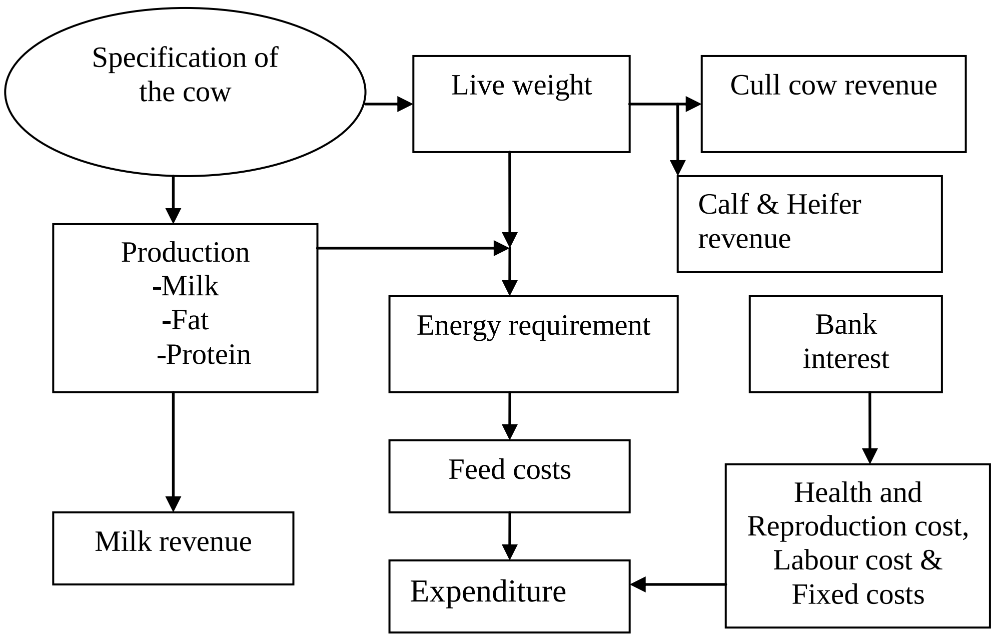


Figure 5.1: Schematic representation of major components of the dairy farm model

5.4 Model structure and programming

Figure 5.2 illustrates the basic structure of the model for dairy farming. It simulates the population dynamics, nutrition, biological and economic performance of the whole farm. Because of the small scale of the enterprises modelled, each animal within the various sex and age classes is accounted for on an individual basis; it is associated with a set of parameters that describe its history, the current state of the cows and their performance. To enable a realistic representation of these small systems, where biological variation is an important practical feature, the main biological events and processes were handled stochastically. Estimates of variations were drawn from survey work (results presented in Chapter 3) and records collected from the Animal Breeding Section at BMPCUL. The models were developed using Microsoft Excel.

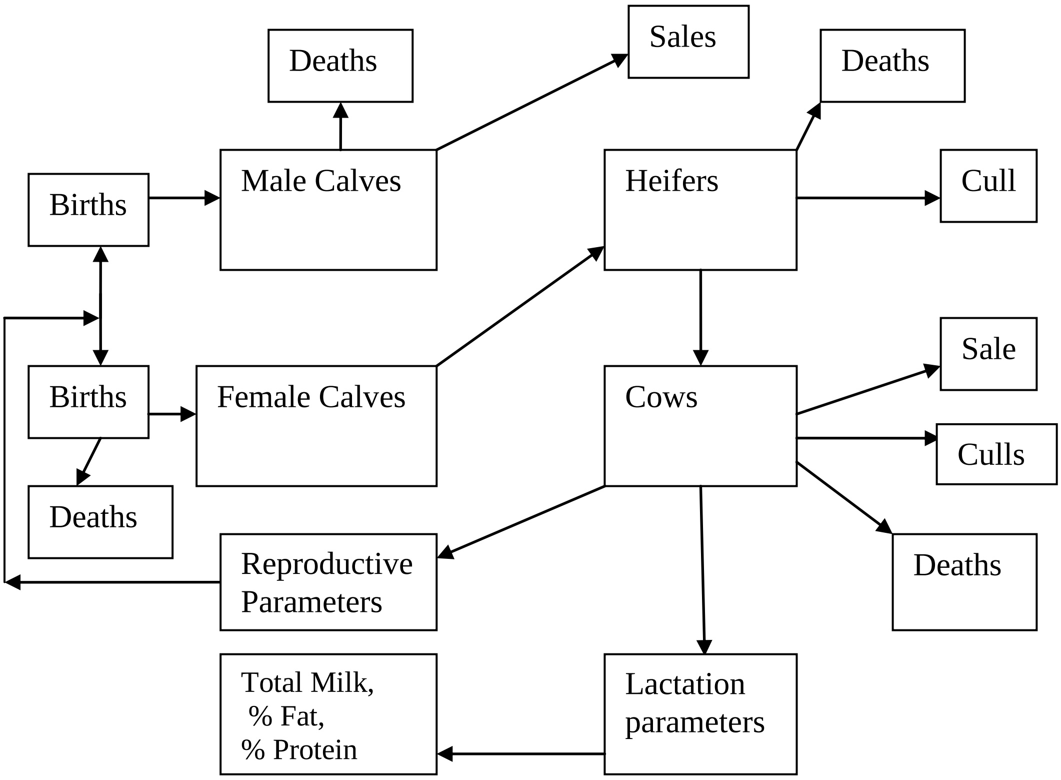


Figure 5.2: Structure of the dairy farm Model

5.5 Herd structure

Livestock activities included in the model are dairying and a dairy-beef-sideline. The livestock classes are calves, heifers, steers and dairy cows. Dairy cow replacements can be reared from the calves born within the herd. However, allowance was made for a small percentage of dairy cow replacements to be bought at the age of sexual maturity. Generally heifers are mated at 2 to 3 years of age to calve at 3 to 4 years of age. The inter-calving interval depends on the genotype of the cows and also the rearing system. In the cooperative dairying system the cows are kept for 10 to 15 years and then sold. Calves can be sold after 1 year of age; however, sometimes they are kept as steers for meat or heifers for replacements.

It was assumed that the herd had 10 age classes: 1 year old (heifers <1 yr), 2 year old (yearlings, 1 to <2) and 3 -10 year old cows from first to 7th lactations. Usually the cows calved initially at 4 years of age, and maintained a calving interval of 388 to 484 days depending on the breeds. Cows were artificially inseminated with semen from the Animal Breeding Section of BMPCUL, and sometimes by natural service with bulls available in the BMPCUL area. Sometimes repeat inseminations were required to achieve a conception rate of 60-70% at the end of mating.

Table 5.1: Survivability of different genotypes in different age groups (information from survey presented in Chapter 3).

Breed	Ages									
group[1]	1	2	3	4	5	6	7	8	9	10
Pabna	0.88	0.87	0.76	0.89	0.92	0.92	0.92	0.89	0.85	0.83
A × P	0.84	0.85	0.74	0.87	0.89	0.89	0.62	0.70	0.67	0.62
H × P	0.85	0.85	0.72	0.85	0.85	0.87	0.87	0.77	0.74	0.72
J× P	0.86	0.87	0.74	0.87	0.87	0.89	0.89	0.82	0.80	0.72
S × P	0.86	0.86	0.73	0.86	0.89	0.89	0.89	0.79	0.78	0.78

[1] P=Pabna, A=Australian-Friesian-Sahiwal, H=Holstein J=Jersey, S=Sahiwal

The calving rate ranged from 50 to 65% (Majid et al., 1998) and the calving rate influened calf survival of the herd. It was assumed that 50% of calves born were males, and that 85% of these survived for selling at 2-3 years of age. In addition, it was assumed that 20% of the male calves were kept as draught animals, and from the female calves, 20-25% were kept for replacements (Khan et al., 2005).

Probabilities of survival were based on the values shown in Table 5.1, obtained from the survey conducted in 2005. Cows remaining in the herd were sold for slaughter or kept as calves for rearing. The proportion (d_j) of the herd in each age class j (j = 1 to

10) was derived from probabilities of survival to the given age class j by the Markov chains (Azzam et al., 1990) as follows:

$$d_j = \prod_{i=4}^{j} s_i / \sum_{k=4}^{10} \prod_{i=4}^{k} S_i$$

where S_i = the probability of an animal surviving from age i to age (i + 1).

k = the age class of cows (4 to 10).

The proportion of animals in age classes 1, 2 and 3 were calculated as: $d_1 = d_2/s_1$, $d_2 = d_3/s_2$ and $d_3 = d_4/s_3$, respectively. s_1=probability of survival from birth up to 1 year, calculated as 1 minus the proportion of rising 1 year olds culled for death, diseases and sales of surplus heifers. Similarly, s_2 = probability of survival from 1 up to 2 years, calculated as 1 minus the proportion of rising 2 year olds culled for death, diseases and sales, and s_3 = probability of survival from 2 up to 3 years, calculated as 1 minus the proportion of rising 3 year olds culled for death, diseases and infertility.

5.6 Stock reconciliation

For a single year of operation, the constraints of the model required that the herd structure was maintained at a ‘steady state’. For example, cow numbers must be maintained by heifer replacements and/or purchases of heifers which must be reconciled (balanced) with cow sales, culling of heifers, death rate and calving percentage. Steer numbers were similarly reconciled. The main features of the model are:

- dairy heifers may be sold, or used as replacements, at the age of sexual maturity
- heifers were calved at 3-4 years of age depending on breed group and the rearing system/management
- death rate of cows was 3 to 5%, depending on age and other factors.

5.7 Feeds and feeding of animals under cooperative dairying

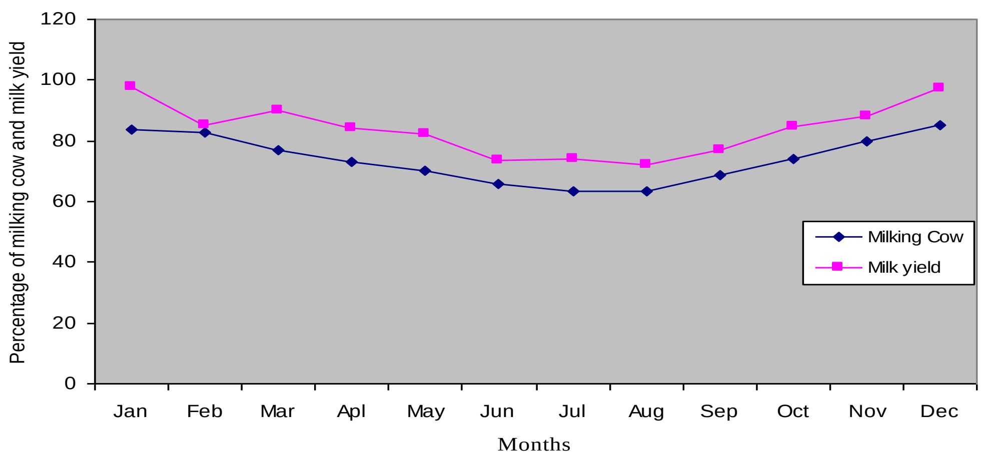
The feeding and management system of cows in the Baghabarighat milk shed area can be classified into two categories: “Bathan” feeding in the dry season (November to April) and stall feeding during the monsoon season (May to October). During the dry period almost all the cattle are grazed on natural pasture named Bathan; in this area, seasonal grasses like *Vigna* spp and *Lathyrus* spp are cultivated. This grazing accounts for almost 1/3 of the required feed for the whole year. During summer (May to September) and the monsoon period, the cattle are fed mainly on straw and hay, conserved from excess grass growth. Some farmers make silage from green pasture.

For the development of the model, it was assumed that throughout the year, roughage consists of about 3% silage and hay, 25-30% pasture and 70% paddy straw (Hossain, 2006). In addition to the Bathan feeding, the cows of this area are fed with 4 to 5 kg straw and 2 to 3 kg concentrates throughout the year. The concentrate mix contains oil cakes, coconut oil cakes, wheat bran, rice polish, keshari bran, brans of grams, mashkalai brans and common salt (Hossain, 2006).

5.8 Number of milking cows and milk yield

Fifty farming families were surveyed from the cooperative dairying area in Bangladesh (Chapter 3). The members of the cooperative supplied their raw milk to the BMPCUL dairy plant throughout the year. However, the number of milking cows and the milk yields fluctuated, depending on the month. In the Baghabarighat milk shed area during the months of November to April, there was sufficient pasture for grazing cows on the Bathan. Therefore, during this period more cows calved. In addition, due to the high quality pasture, milk production was also higher in these months than at other times. Figure 5.3 shows the percentage of cows in milk, and the total potential milk yield (%) throughout the year in Banghabarighat milk shed area.

Figure 5.3: Milking cows (%) and total milk yield (%) throughout the year in Baghabarighat milk shed area in 2005



5.9 Birth weight

Calf birth weight (Wc) can be calculated from the equation of Roy (1980):

W_c (kg) = $(W_m^{0.73} - 28.89)/2.064$

where W_m is the mature body weight of the dam.

5.10 Liveweight (LW)

The liveweight at age t in days (W_t) was calculated using the von Bertanlanffy equation as given by Bakker and Koops (1978):

$$W_t = W_m \{1-[1-(W_o/W_m)^{1/3}]e^{-kt}\}^3$$

where W_m = mature liveweight , W_o = birth weight, k = constant related to rate of maturation, and e = base of the natural logarithm.

5.11 Description of cow requirements model

The energy requirements of cows were determined by accounting for mature liveweight (LW), milk yield (MY), fat yield (FY) and protein yield (PY) as proposed by AFRC (1993) and Lopez-Villalobos et al. (2000).

5.12 Energy and dry matter requirements

The farmers of the cooperative dairy industry fed their cows both roughages and concentrates as noted above in section 5.7. It was assumed that the roughage and concentrate mix contained 18.6 MJ gross energy and 10.5 MJ metabolisable energy (ME) per kg dry matter (DM) (Holmes et al., 2002).

The corresponding metabolisability of the feed at maintenance (q_m) was 0.59. The efficiencies of utilisation of ME were calculated as defined in AFRC (1993).

Efficiency for maintenance	$k_m = 0.35q_m + 0.503 = 0.71$
Efficiency for lactation	$k_l = 0.35q_m + 0.420 = 0.63$
Efficiency for growth of lactating cows	$k_g = 0.95k_l = 0.59$
Efficiency for growth of growing replacements	$k_f = 0.78q_m + 0.006 = 0.47$
Efficiency for growth of conceptus	$k_c = 0.133$.

5.13 Cow maintenance

The ME requirement for the maintenance (MEm) of cows was calculated in 1-month period within the production year as:

ME_m (MJ/d) = $(F_m+A_c)/k_m$

where F_m is the fasting metabolism = $30.5\{0.53(W_t/1.08)^{0.67}\}$

and A_c is the activity allowance, $A_c= 0.0095\ W_t$.

The activity allowance was calculated assuming that a cow walked approximately 3 kilometres during grazing (AFRC, 1993) and W_t = average weight over the 1 month period.

Table 5.2: Herd-level production variables

Variables	Genotypes				
	P	A × P	H × P	J × P	S × P
Birth wt (kg)	22[5,8]	21[3,8]	27[2]	22[8]	27[7]
Mature LW (kg)	247[1,8]	353[8]	375[6]	307[8]	307[8]
Gestation period (d)	280[4,8]	280[4,8]	278[4,8]	280[4,8]	279[1,8]
270-days milk yield (kg)	1697[*]	2188[*]	1993[*]	1635[*]	1823[*]
270-days protein yield (kg)	65[**]	78[**]	66[**]	55[**]	66[**]
270-days fat yield (kg)	74[*]	77[*]	77[*]	64[*]	75[*]
Calving Interval (d)	484[4]	450[4,8]	386[4,8]	390[4,8]	479[3]
Milk yield (kg/year)	1280	1775	1885	1530	1389
Protein yield (kg/year)	49	63	62	53	50
Fat yield (kg/year)	56	62	73	60	57
Calving rate	0.65[1]	0.55[5]	0.55[5]	0.52[3]	0.60[3]
Survivability up to 1 year	0.88[8]	0.84[8]	0.85[8]	0.86[8]	0.86[8]
Productive life time (Years)	7.54[8]	8.11[8]	9.46[8]	9.36[8]	7.62[8]

Legends:P=Pabna, A=Australian-Friesian-Sahiwal, H=Holstein, J=Jersey, S =Sahiwal

[1]Islam et al., 2004; [2]Hirooka and Bhuiyan, 1995; [3] Nahar et al.,1992; [4] Majid et al.,1998; [5] Khan et al., 2000; [6] Ahmed and Islam,1987; [7]Islam and Bhuiyan, 1997; [8]Chapter 3 ; [*] Chapter 4 (from Nelder model) and (**) was calculated from the total lactation yields and protein percentage.

5.14 Cow growth

Liveweight was predicted over 1 month intervals from 48 months to 120 months (10 years) of age. The liveweight gains (LWG) of growing lactating cows were assumed to be linear between adjacent monthly weights. The metabolisable energy required for growing lactating cows was calculated as:

$ME_g = (LWG \times EV_g)/k_g$,

where EV_g = energy value of 1 unit of LWG calculated as:

EV_g (MJ/k_g) = $\{1.3\ (4.1+0.0332W_t - 0.000009W_t^2)\}/\{1\text{-}0.1475LWG\}$

5.15 Cow gestation

Gestation length of the various genotypes ranged from 278 to 280 days (Majid et al., 1998; Khan et al., 2005). Requirements of ME to maintain pregnancy (ME_c) were calculated as follows:

$ME_c = EV_c/k_c$,

where k_c Efficiency for growth of conceptus (k_c = 0.133).

and EV_c (MJ/d) = $0.025W_o\ (E_t\ 0.0201^{e\ -0.0000576t})$

EV_c = retained energy in the foetus and E_t = total energy retention at day t of gestation derived from log10 E_t (MJ/d) = $151.665 - 151.64^{\ e-0.0000576t}$.

5.16 Cow lactation

The net energy value of milk (EV_l) was predicted for each age class using the formula of Tyrell and Reid (1965) as below:

EV_l (MJ/kg) = 0.0376F + 0.0209P + 0.948

where F and P are fat and protein yield, respectively. The requirements of ME for lactation can be determined as:

ME_l (MJ) = EV_l/k_l.

In order to calculate the net energy in the milk, the milk production and the milk fat and protein concentrations, over the entire lactation period had to be estimated. In chapter 4, the Nelder model (Nelder 1966) was shown to be the best mathematical model in predicting lactation yield:

$$\frac{t}{Y} = a + bt + ct^2 + dt^3$$

Where Y = Milk yield (kg/d)

t = time of lactation

The a, b, c and d (intercept, curve shape and placement of parabola, respectively) parameters can be calculated from the expected yield and the days in milk.

The input parameters were derived after fitting the Nelder model and are presented in Table 5.2. The predicted 270-days lactation yields were considered as the yield per calving interval and this yield was expressed as per year (Table 5.2). The predicted protein yield was calculated from the lactation milk yield and protein percentage value as detailed found in the published literature.

5.17 Calf requirements

Energy requirements for maintenance and LWG (ME_{mp}) for replacements were adjusted for feeding levels (AFRC, 1993). Liveweights were predicted over 1 month periods, from birth up to 36 months of age, and the LWG (E_f) was scaled to the energy required for maintenance (E_m) as:

$R = E_f/E_m$

where E_f and E_m were calculated as:

E_f (MJ/d) = 1.10 (LWG $\times$ EV_g) and

$E_m = F_m + A_c$

where $A_c = 0.00009W_t$.

The ME_{mp} was calculated as:

ME_{mp} (MJ/d) = (E_m/k_r) In {B/B-R-1)}

where $k_r = k_m \times$ In (k_m/k_f) and B = $k_m/(k_m-k_f)$.

Where R is the retention of net energy, B and k_r are the factors, being directly related to q_m and ln is the natural logarithm.

The calves were either kept as replacements for culled cows, or for sale at 1-2 years of age. Milk produced in the first 5 days after calving is colostrum which is unsaleable and fed to the calves. Each calf was assumed to eat 20 kg DM of meal

during the first 60d of life (Lopez-Villalobos et al., 2000). Requirements for milk were calculated as the difference between the total energy required and the energy supplied by the meal. The quantities of milk, fat and protein fed to calves were accounted for in determining the sale value of milk produced by the herd.
Total herd requirements for ME were calculated as:

$$ME_{herd} = \sum ME_{totalj} \times d_j$$

Where, J= 1 to 10 years and dj is the number of animals in each age class.

Requirements for DM were calculated by dividing ME_{herd} by the ME content per kg pasture DM. It was assumed that animals could at all times consume the pasture needed to meet their specified energy demands. Requirements for DM per cow, included DM for growing of replacements, and was calculated by dividing the total requirements for DM of the whole herd by the number of cows older than 3 years, because in the milking herds the cows were milked from age 4 to 10 years of age.

5.18 Stocking rate

Throughout the year, lactating cows are fed 2-3 kg/day/cow of concentrates (Hossain, 2006). The stocking rate, defined as the number of cows grazing per hectare, was assumed to be 6,000kg of DM/total DM required per cow, following Lopez-Villalobos et al. (2000). This calculation assumed that the number of animals grazed per hectare was adjusted to meet the DM requirements, which in turn were determined by the production levels of the animals.

5.19 Biological efficiency

The feed dry matter required for lactation, divided by the total dry matter requirement of a cow, provides a measure of biological efficiency.

5.20 Economic analysis

The economic analysis was based on average values of marketable products and costs of Bangladesh dairying under a cooperative system. In this study, the profit was derived from the differences between revenue (R) and costs (C). Profit is expressed through grouping terms by the class of cattle, and calculating revenue together with costs per cow per year.

5.21 Revenue

Income was derived from the sale of milk, calves, culled heifers and cows as well as revenue from draft animals and manure. The revenue (R) per cow per year is calculated using the equation:

$$R_{total} = R_{calves} + R_{culledheifers} + R_{culledcows} + R_{milk} + R_{draught} + R_{manure}$$

The detailed procedures to estimate the income are described as follows:

5.21.1 Revenue from calves

For estimating revenue from calves, the number of cows calving per year, calving rate, survivability up to 1 year, and the yearling price of both male and female calves were considered.

$$R_{calves} = \left(NoC_{peryr} \times CR \times S \right) \times \frac{(P_{mcalf} + P_{fcalf})}{2}$$

Where NoC_{peryr} = Number of calving per year = 365/calving interval

CR = Calving rate

S = Survivability up to 1 year

P_{mcalf} = Price of yearling male calf

P_{fcalf} = Price of yearling female calf

5.21.2 Revenue from culled heifer

For estimating the revenue from culled heifers, the number of female calves per cow per year, liveweight of the calves at the time of culling and price per kg liveweight were considered.

$$R_{culled\ heifer} = (Nof_{calves} percow/yr) \times LW_{heifer} \times P_{kg}$$

Where, $R_{culled\ heifer}$ = Revenue from culled heifers

Nof_{calves} per cow/yr= Number of female calf per cow per year

LW_{heifer} = Liveweight of heifer at the time of culling

P_{kg} = Price per kg liveweight

5.21.3 Revenue from culled cows

The revenue from cull cows is calculated according to the following formula.

$$R_{culledcows} = LW_{atcullingperproductivelifetime\,(yr)} * P_{perkgLW}$$

where, $R_{culledcows}$ = Revenue from cows culled at old age

$LW_{atcullingperpropductivelifetime\,(yr)}$ = Liveweight at the time of culling/productive lifetime (year)

$P_{perkgLW}$ = Price per kg liveweight.

5.21.4 Revenue from sales of milk

Under the cooperative dairying the farmer members pool their milk at the primary dairy cooperative society, which then arranges regular cash payments based on milk volume and fat percentage. However, payment of milk paid ultimately to members, is based on milk volume only. In the current payment system, the total fat and protein production was not considered. In the formula, the milk income is adjusted to 4 percent fat and 3.5 percent protein. So in estimating the revenue from milk sales, the average price per kg of milk was used, and the fat and protein value was set to zero (0) to reflect current market conditions.

$$R_{milk} = MY * P_{perkgmilk} + TFY - (MY * 0.04) * P_{perkgfat} + TPY - (MY * 0.035) * P_{perkgprotein}$$

Where, R_{milk} = Revenue from sale proceeds of milk

MY= Yearly milk yield

$P_{perkgmilk}$ = Price per kg milk

TFY=Total fat Yield

$P_{perkgfat}$ = Price per kg fat (0)

TPY = Total protein yield

$P_{perkgprotein}$ = Price per kg protein (0)

.21.5 Revenue from draught

Under the cooperative dairying system, the farmers have cultivable land on which they grow paddy, seasonal crops, vegetables and fodder. Moreover, some farmers sell their draught power to other farmers for cash. For estimating the revenue from draught, it was assumed that there are 6 working hours per day and, the farmer uses draught for 150 days per year, which including both days sold, and utilised on his own farm. The cost per hour was assumed to be 20 Taka.

$$R_{draught} = W_h \times P_{perh} \times (NoWd_{peryr})$$

Where

W_h= Working hour

P_{perh} = Price per hour

$NoWd_{peryr}$ = Number of working days per year

5.21.6 Revenue from manure

The manure revenue per farm per year was assumed to be 20,000.00 Taka (Chapter 3). However, some farmers sell their manure while others use it on their cultivable land or alternatively, use it as fuel. Therefore, the average value of manure revenue was considered in this model.

5.22 Costs

Costs (C) will be derived from the following equation:

$$C_{total} = C_{calves\ feeding\ cost} + C_{heifer\ feeding\ cost} + C_{cow\ feeding\ cost} + C_{dry\ cow\ feeding\ cost} + C_{heifer\ health\ cost} + C_{cow\ health\ cost} + C_{cow\ production\ cost} + C_{labour\ cost} + C_{milk\ marketing\ cost} + C_{fixed\ cost}$$

5.22.1 Feeding costs

The unit prices and costs are presented in Table 5.3. The daily animal energy consumption was calculated from the daily energy requirements, and taking into account the effects of liveweight changes. Daily feed costs were based on a mixed intake of roughage and concentrate. The concentrate mix includes rice polish, wheat bran, oilcakes and common salt. Metabolizable energy requirements were allowed for maintenance, production and pregnancy (AFRC, 1993) assuming an energy density in the feed of 10.5 MJ of metabolizable energy/kg DM. Feed costs were assumed to be 6.0 Taka per kg DM over a representative mix of both roughages and concentrates. The assumed price of green grasses was very low, and the price of roughage based solely on the price of paddy straw. The concentrate price accounts for the different prices of the various brans used in the ration, and this price was similar to that reported by Khan et al., (2005).

5.22.2 Health costs

Management practices such as drenching, dipping, vaccination and de-worming were undertaken on most of the farms. Cow health costs were 3500 Taka for each cow of the Pabna, Sahiwal × Pabna, Jersey × Pabna and Australian-Sahiwal-Friesian × Pabna genotypes and 4000 taka for Holstein-Friesian × Pabna crossbred animals.

5.22.3 Labour costs

For hired labour, cash labour costs incurred in 2005 were used. For unpaid family labour, the average wage rate per day for a qualified full-time worker in the respective region was used. It was assumed that a labour unit can look after 10-12 milking cows in a day and labour costs calculated to be 2920 Taka per cow per year.

Table 5.3: Unit prices and costs (Based on information presented in Chapter 3)

Prices	Bangladeshi Taka
Milk price per kg	25.00
Fat price per kg	0
Protein price per kg	0
Live animal cost per kg	100.00
One year old calf price	2500.00
Two year old female calf price	2000.00
Concentrate per kg	10.00
Natural pasture silage per kg DM	4.00
Straw per kg DM	1.50
Heifer health costs per head per day	2.00
Cow health costs (varies with genotypes) per head per year	3000.00 – 4000.00
Heifer and cow reproduction costs per head per year	1000.00
Fixed cost per head per year (varies with genotypes)	2000.00-2500.00
Labour cost per person per day	60.00

* 1US$=BDTk 70.00

5.22.4 Capital recurrent costs

In regard to land, it was assumed that farmers have their own land for dairy cattle rearing. Capital was defined as assets, without land and quota, plus circulating capital. Farmer’s borrowed money for cattle rearing from the state ownered banks, commercial banks, NGOs (e.g. Bangladesh Rural Advancement Committee, BRAC) and private banks (e. g. Grameen Bank). The interest rate of the state owned bank was lower (6%) but the interest rates of the other private bank were higher (18%) and they collected the lending money as installments basis (Shamsuddin, 2005). Therefore, for borrowed funds an average real bank interest rate of 12 percent was used.

5.22.5 Fixed costs

Other operational costs were assumed to be fixed costs and varied from 2000 to 2500 Taka per cow per year on the basis of genotype (Chapter 3). Apart from costs incurred by the producer, including those attributable to equipment, machinery and farm structures (fixed costs), all other costs were variable as they were influenced by the level of herd production.

5.22.6 Marketing costs

For marketing in the cooperative system, BMPCUL ensures a regular collection of milk from their cooperative members. For transporting the raw milk from the primary societies collection point to the milk plant, BMPCUL deducts 0.20 Taka per kg of milk per year. After collecting the raw milk, it was transferred to processing plants for pasteurisation and packaging. The packaged milk was then sold to distributors in turn sell to the end consumers. Any surplus earned by the central dairy cooperative through marketing milk and milk products, was paid back to the members. Some commercial farmers supplied their milk to the cooperative plant and, some sold their milk to the middle man; who collects it from the farmers, and sold it to the end consumer and/or milk processing company.

BMPCUL provides all the necessary support services to farmer members for animal breeding, feeding, health and training in animal management.

The cost of the bull calf marketing was negligible because most of the time, the middle man purchased the bull calf from the farmer’s house, or sometimes the farmer sold it directly at the village markets.

In this analysis, the costs for land, house and cow purchases were not considered for estimating profit. Only operational costs were considered within current market values. No allowance was made for seasonal variation of prices in this analysis, although all input variables were considered to be constant throughout the year.

5.23 Results

5.23.1 Costs, feed requirements, revenue and profit

Table 5.4 shows the costs, revenue and profit of five cattle genotypes under cooperative dairying in Bangladesh, calculated from the current model. Total revenue was dominated by the sale of milk (82 – 85%) and beef (15 – 18%). Feed costs accounted for 64-69% of the total costs. Health costs, reproduction costs, labour costs, marketing costs and all other operational and management costs were assumed as fixed costs. Cow and heifer rearing costs were 31-36% of total cost.

Pabna cattle had the lowest DM requirements, while Holstein × Pabna, had the highest total DM requirements. Other genotypes had intermediate DM requirements. Overall, Pabna cattle were the least costly, while the Australian-Friesian-Sahiwal × Pabna genotype, the most costly to farm. However, the Holstein × Pabna genotype had the highest milk and beef revenue; that is, this genotype generated the highest profit than other genotypes.

The values for biological efficiency for Pabna, Holstein × Pabna, Sahiwal × Pabna, Jersey × Pabna and Australian-Friesian-Sahiwal × Pabna cows are presented in Table 5.4. Table 5.4 indicated that temperate breed crosses showed higher profit than tropical breed and their crosses e.g. Holstein × Pabna crossbreds produced the highest and Pabna cattle produced the lowest profit, whilst all other genotypes produced intermediate profit. Nevertheless in the case of biological efficiency, the reverse results were obtained; that is, Pabna cattle exhibited the highest and Australian-Friesian-Sahiwal × Pabna the lowest.

5.23.2 Total farm income

The income per year for a 100 cow dairy herd consisting of a mixture of Pabna cattle and its crossbreds is shown in Table 5.5. The herd composition was considered in this model to reflect real breed composition in a typical dairy herd under the BMPCUL, based on the results of the survey presented in Chapter 3. The predicted net annual income for a 100 cow dairy herd was US$ 20,297. Milk income comprises approximately 97% of the total farm income per year.

Table 5.4: Feed requirements, costs, revenue and income from different breed groups

Traits	Breed group				
	Pabna	H × P	S × P	J × P	A × P
DM requirement per cow per year (kg)					
Maintenance	1053	1414	1228	1228	1355
Lactation	435	641	473	534	603
Gestation	139	164	167	139	133
Total DM requirement	1627	2219	1868	1901	2091
DM requirement for calves (kg/head/year)					
Calves (Male + Female)	1686	2292	1936	1941	2167
Total DM requirements (kg/year)	3313	4511	3804	3842	4258
Total feed costs (Tk)	19878	27066	22824	23052	25548
Heifer health cost (Tk)	1460	1460	1460	1460	1460
Cow health cost (Tk)	3500	4000	3500	4000	4000
Cow Reproduction cost (Tk)	800	1200	900	1000	1200
Labour cost (Tk)	2920	2920	2920	2920	2920
Marketing cost (Tk)	267	349	271	289	309
Fixed cost (Tk)	2000	2500	2200	2500	2500
Grant total (Tk) costs	30825	39495	34075	35221	37937
Revenue/Income					
Calf revenue (Tk)	1493	1787	1474	1790	1570
Cull cow value (Tk)	3275	3966	4029	3196	4352
Heifer revenue (Tk)	2074	2600	2096	2574	2231
Milk value (Tk)	31994	47114	34728	39262	44368
Manure+Draughtrevenue (Tk)	58	40	47	30	39
Grand Total revenue	38894	55507	42374	46852	52560
Net Income (Tk)	8069	16012	8299	11631	14623
Net Income,US$	115	229	119	166	209
Biological Efficiency	15.77	14.98	13.75	14.50	13.59

Legends: P=Pabna, A=Australian-Friesian-Sahiwal, H=Holstein J=Jersey, S=Sahiwal

Table 5.5: Net farm income per year for a mixed herd[1] of 100 cows

Item	Value
Feed	1,227,697
Heifer health	26,849
Cow health cost	369,420
Reproduction cost	99,590
Labour cost	290,803
Marketing cost	30,014
Fixed cost	226,229
Grand total	22,70,602
Income from calf	63,375
Income from heifer	7,513
Income from manure	20,000
Income from cull cows	10,746
Income from milk	3,751,789
Grand total	3,833,422
Draught income	18,000
Bank Interest	180,000
Net income (Taka)	1,420,820
Net income ($US)	20,297

[1]Mixed herd comprises an average 27% Pabna, 9% Australian-Friesian-Sahiwal × Pabna, 12% Jersey × Pabna, 31% Holstein × Pabna and 21% Sahiwal × Pabna.

5.23.3 Capital investment returns

Most farmers have their own land for rearing their cows. In the current model, the simulated 100 cow dairy herd required 7.8 hectares of land and the total land value was about US$10,582. The total value of assets (the sum of land value, market value of 100 cows and the cost of building and machinery) was approximately US$14,286. On the whole farm basis, land is the most important asset, given that land prices are very high. Therefore land values represent between 60 and 68% of the total farms assets. Cattle comprise the second most important asset, varying from 20 to 30 % of the farms asset value. Machinery, buildings and cash in hand are combined as other assets, and make up between 9 to 11 % of the value of total farm assets. The capital investment returns of different cow genotypes are presented in Table 5.6.

Table 5.6: Capital investment returns (US$) per 100 cows

Items	Breed groups				
	Pabna	H × P	S × P	J × P	A × P
Cost of animals	28,571	42,857	35,714	35,714	40,000
Total assets	125,502	139,788	132,645	132,645	136,931
Total Income	11,241	23,160	11,713	16,616	21,176
Return from dairy farming (%)	9.0	16.6	8.8	12.5	15.5

5.24 Discussion

The management of a dairy farm is a complex operation. The numerous combinations of management options, combined with variability in climate, markets and financial scenarios, dictate that superior strategies for each individual farming system could never be determined experimentally in the field. Simulation modelling offers the only realistic method of integrating and estimating these effects. The whole farm model could be used to assist with optimisation of farm profitability (Mayer et al., 1998), but since it is a simulation of reality, the results must be treated with caution, and excessive inference avoided.

5.24.1 Model establishment

In the present simulation model, animal population dynamics, aspects of animal biology, farm costs and the revenue of an average dairy farm operation under cooperative dairying were considered. The input parameters of this model were taken after fitting the best lactation mathematical model (Nelder model) in chapter 4 and other values were obtained from the survey of cooperative dairy farms of 2005 (Chapter 3). The model was constructed using partial budgeting, whereby the system under study was represented by a framework of mathematical equations. Verification of how well the simulation model represented the performance of real farms could be investigated by applying data to the model from farms not used to establish the model. However, records from alternative farms were not available from the BMPCUL region. Therefore, validation of the model was restricted to the comparison of current results, with those reported from other investigations.

5.24.2 Costs, revenues and profits

In the model, income was derived from milk, beef, draught and manure, while expenses included: feed costs, health costs, reproduction costs, labour costs, marketing costs; and all other operational and management costs considered as fixed costs. The current Bangladeshi milk payment system, which is based on milk volume only, was used to calculate profit. Hence, the individual cow’s lactation milk yield, feed cost, liveweight and prices of milk yield greatly affected the model output, and thus impacted on the fixed parameters. Therefore, the effects of these factors on model output were investigated as below.

The dry matter (DM) requirements for maintenance, growth of replacements and lactation, were lower for Pabna cattle than other genotypes due to lower body weight. Nevertheless the Holstein × Pabna genotype is heavy, so its DM requirements were higher than other light genotypes. However, this genotype contributed higher beef income than other genotypes. The body weight of the cow is important as it affects the profitability and consequently its effects on feed requirements for maintenance as well as the value of the carcass. Similar findings were reported by Lopez-Villaobos et al. (2000). In this model, feed costs accounted for 64-69% of the total costs while the remaining percentage was other operational costs. Similar findings for feed costs of total costs for dairy farm operation were reported by other workers (e.g. Moran, 2005). However, Ozawa et al., (2005) reported 4 to 9% higher feeding costs in Hokkaido dairy farm than the current study.

The estimated cow biological efficiency (DM for lactation as a proportion of total DM) was highest in Pabna cattle (15.8%) and lowest in Australian-Friesian-Sahiwal × Pabna and Sahiwal × Pabna genotypes (both 13.6%). Lopez-Villalobos et al. (2000) reported that Holstein-Friesian × Jersey, Jersey × Ayrshire and Holstein-Friesian × Ayrshire genotypes produced 39.1%, 39.1% and 37.9% biological efficiency, respectively. Biological efficiency was calculated at 55-67% for Jersey cattle and 55-61% for Holstein cattle after feeding total roughage, and roughage and 50% concentrates (Oldenbroek 1986; 1988). The results obtained from this study were much lower than those previously reported. This may be attributed due to the low lactation yields of Bangladeshi dairy cattle, poor feeding and management and it was also indicated that these cattle produce milk less efficiently.

To derive net income the average price of milk at 25 Taka/litre, feed price of 6.0 Taka per kg DM over a representative mix of both roughages and concentrates, and meat price of 100 taka/kg, were used. These figures are based on survey work (Chapter 3 and BBS, 2005). However, the prices of each parameters varies by region, and manufacturing factory. A sensitivity analysis a 20% price variation of milk, feed costs, expenditure and beef price is presented in Chapter 6.

The net annual profit of different genotypes ranged from US$115 to US$229 on a per cow per year basis. Similar net profits (US$159 per cow per year) were reported for Bangladeshi government farms operating with a 25% subsidy, irrespective of breed groups (Rahman et al., 2003).

The profitability of the Holstein × Pabna genotype was the highest of all five genotypes studied. The profitability of the two temperate by tropical crossbreds was intermediate, with the two tropical genotypes being the lowest. These results are consistent with those reported by Gunjal et al. (1997), Kahi et al. (2000) and Khan et al. (2005). The higher profitability of the temperate genotypes is driven by their higher genetic potential for milk production. The higher relative milk production of Holstein × Pabna cows is reflected in the higher milk revenue: feed cost ratio; 1.74 in comparison to 1.61 for Pabna cows.

However, it has been reported that while first-generation crossbred dairy cows produce good financial returns in tropical countries, poorer results are found in the subsequent generations (Cunningham and Syrstad, 1987). This phenomenon is most likely due to the deterioration of fertility, and increased in mortality in second and later generation cross-breds, due to poor adaptation of temperate genotypes to tropical conditions.

Although it was reported from current and other studies, that the High Yielding Varieties (HYVs) of livestock showed higher profitability than local breeds, Hemme et al. (2004) obtained lower profitability from small scale farmers under dairy production in Bangladesh, their studies indicated low productivity due to high mortality and low utilisation rates of HYVs. Therefore it was clear that the HYVs contributed to higher economy in livestock production in Bangladesh.

5.24.3 Total farm income

The annual profit for a 100 cow mixed-breed herd consisting of Pabna, Australian-Friesian-Sahiwal × Pabna, Jersey × Pabna, Holstein × Pabna and Sahiwal × Pabna respectively was calculated as US$20,000. Similar results were found when the profit from a mixed farm with Pabna cattle under cooperating dairying in Bangladesh was calculated (Udo et al., 1992). In contrast, Hemme et al. (2004) showed that returns from farming mixed herds in Bangladesh ranged from US$1,362 to US$16,576 per year. The profit from the dairy enterprise component of the farms reportedly ranged from 20 to 76% of the total profit compared to 82 to 85% from the current model. Hemme et al. (2004) stated that farm income was highly dependent on the number of milking cows on the mixed farm, and the level of feeding concentrates. The difference might be accounted for by the fact that Hemme et al. (2004) calculated profitability from mixed farms with a lower herd size, and considered the lower operational costs in their model.

In the current study, feed costs (54% of total operational costs) were lower than reported in other studies (e.g. Rahman et al., 2003) because they considered feeding only concentrates to the cows. About 5 to 7% lower feeding costs was obtained in the current study than that of Rahman et al. (2003) because feeding costs in the current study can be attributed to *Bathan* feeding, which was not valued under cooperative dairying.

5.24.4 Income from draught and manure

In the mixed farming system, the main function of keeping cattle is to provide additional income, or provide draught and manure for crop growing. Cattle density, an index of draught power and the amount of manure available per hectare, is correlated positively with the level of cropping. Draught animals also supply a small amount of cash income if such draught power is sold to other farmers. For mixed enterprise farms, manure is often considered to be one of the main benefits of farming cattle (Udo et al., 1992). In this study, the role of cattle in providing draught and manure was found to be very low in economic terms. This low income existed because usually, the milking cows were kept for milking purposes only, manure being used to increase the soil fertility, only a small number of milking cows were used for draught purposes, and sometimes a small portion of manure was sold.

5.24.5 Return on investment

In this analysis, it was shown that the return on capital investment was highest for the Holstein × Pabna genotype (16.6%) and lowest for the Sahiwal × Pabna genotype (8.8%). The highest return on capital investment of Holstein × Pabna was attributed to the milk yield of this genotype being higher than other genotypes. The return on investment depends on accurate data combining physical and financial information, farming systems, efficient farm management, prices of land and machinery and production from animals. Similar factors were reported by Attrill (2000) for estimating the return on investment from dairy farming in a New Zealand. Furthermore, the return on investment of different genotypes in the current study was similar with the results of Attrill (2000), who observed the return on net operating assets for owner-operators ranged from 0.08% to 21% for the period 1993/94 to 1998/99 in a New Zealand study. There are no proper reports of return on investment for dairying and other agri-business available in Bangladesh currently.

5.24.6 Limitation of the current model

In the development of the model, the milking cow’s age was considered from 4 to 10 years old. However, sometimes farmers continue to milk cows older than 10 years. For developing this model the practical aspect of cow’s age was not considered. Rather, a fixed age structure (from 4 to 10 years) was used. In this model, the number of animals grazed per hectare was adjusted to meet the DM requirements, which in turn were determined by the production levels of the animals. DM requirements were set at 6000kg DM required but in practice this figure is variable and hence affects the outputs of the model.

5.25 Conclusion

A deterministic simulation model that reflected the outputs of real dairy farms in the BMPCUL region was developed. The study showed that relative to local genotypes, temperate breeds which are genetically superior in terms of milk production, created a higher income for dairy farmers. Although the first generation temperate crossbreeds also generated greater feed costs, the net profit associated with these breeds was higher than for tropical breeds. However, survivability of Pabna and

Sahiwal × Pabna genotypes was better than temperate crossbreeds under cooperative dairying in Bangladesh.

In this simulation study it was seen that the dairy farm operation under cooperative dairying was indeed profitable. The return on investment from dairy farming was competitive with other investment opportunities. The model developed in this study could well assist farmers and policy makers to make more informed decisions regarding the dairy farming sector. It will also assist researchers interested in conducting further research under the cooperative dairying system in Bangladesh.

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CHAPTER SIX

Economic Values for Traits in the Breeding Objective and Prediction of Genetic Gains

6.1 Abstract

A breeding objective was developed for cooperative dairying conditions in Bangladesh. The traits considered were milk yield, fat yield, protein yield, calving interval, liveweight, birth weight, survivability and calving rate. A linear profitability model was developed based on the relationship between average performance levels for the traits, and the levels of output from the farm. The total annual profit of the herd was derived from the difference between costs and revenue. The annual profit per cow per year, was highest for Holstein × Pabna (US$246.41) and lowest (US$101.70) for Pabna. There were no differences in economic weights (US$0.32) of milk yields for various genotypes on a per cow per year basis. Economic values of fat and protein were negative, due to there being no payment to farmers for the fat and/or protein yield. Economic values of mature liveweight for different genotypes ranged from -US$0.39 to -US$0.27 on a per cow per year basis to -US$0.18 to -US$0.13 on a per ton of feed DM basis. Economic values for birth weight were also negative, with a one kg increase in birth weight, decreasing income from -US$0.49 to -US$ 0.05 on a per cow per year basis and from -US$0.17 to -US$0.03 on a per ton of feed DM basis. Economic values of calving interval and calving rate were negative for all the genotypes. The economic values for survivability had a positive impact on farm profit due to the changing herd composition, and increased milk output. Sensitivity analyses changed the base price of feed, milk, beef and fixed costs by ±20% the future direction of genetic improvement to be examined. It shows that the economic values for responsive traits (fat yield, protein yield and calving interval) may change, depending on prices levels. The selection index weightings for milk yield were positive for all genotypes, while those of the protein yield were negative. The higher predicted genetic gain for Pabna cattle in the objective was 49.7i per standardised selection differential than other genotype. Selection of cows on the basis of milk volume was more profitable than selection on total fat and protein yields.

(**Key words:** Profit equation, genotypes, breeding objectives, economic values, selection index)

6.2 Introduction

The density of dairy cattle in Bangladesh is higher than in some developed countries of the world. For example, there are over two and half times as many cattle in Bangladesh as there are in New Zealand, which is one of the major exporters of dairy produce worldwide (Hemme et al., 2004). The average milk production per cow per year is an estimated 2190 kg in developed countries, 1220 kg in Asia, whereas it is only 206 kg in Bangladesh (Ali and Ali, 2003). This low productivity is due to a combination of poor genetic potential, inadequate nutrition, and poor management.

There are about 40,000 small holding dairy farmers who are the members of the Bangladesh Milk Producer's Cooperative Union Limited (BMPCUL). They supply more than average 200,000 litres of liquid milk daily to the BMPCUL dairy plant. Most of the farmer members are dependent solely on income from their cattle farming, and would benefit substantially financially from higher milk yields being generated from more suitably improved cattle genetics.

At present, there is a great shortage of milk and meat being produced in Bangladesh (FAO, 2004). This shortage of milk and meat contributes to the low nutritional status of the Bangladeshi people. Relieving the milk shortage in Bangladesh require efficient planning within the entire industry, employing consistent objective breeding decisions aimed at genetically improving the dairy cattle.

Definition of the breeding objective should be the primary step in the development of a structured breeding programme (James, 1982; Harris et al., 1984 and Ponzoni, 1986). Breeding objectives should align closely with the overall objective of the livestock business in which animals are used, as they are the critical link using genetically improved animals (Amer et al., 1998). The breeding objective is defined as a combination of economically important traits of dairy cattle within the production system. Breeding objectives should account for inputs, such as food, husbandry and marketing costs, as well as for outputs, such as income from milk and beef sales. Decisions on which traits are to be included in the breeding objective should be based on economic grounds and on whether they are difficult or easy to measure or to change genetically.

The aim of genetic improvement of livestock is to create successive generations of animals capable of producing the desired product more efficiently under future farm economics and social circumstances, than those of the present generation of animals (Groen, 2000). Performance varies widely between animals, due to the differences of genetic makeup in each individual, effects of management practices, and also environmental conditions. Generally, animals rank in different order for different traits, so in practice, it is best to choose animals based on the aggregation of several traits (Hazel, 1943). One approach is to combine all traits into an index which is called the selection index (Smith, 1936 and Hazel 1943). The traits in the index differ in variability, heritability, and in correlation between the phenotypes and genotypes of the traits (Turner and Young, 1969). The use of a selection index is more effective in generating genetic change than other methods of selection (Hazel and Lush, 1943 and Hazel et al., 1994).

Specification of the breeding objective, requires the calculation of economic values for all traits having an impact on profitability (James, 1982). Traits of interest for dairy farmers include milk, fat and protein yield, calving interval and survivability. The economic values for milk production traits have been widely discussed in the literature (Beard, 1988; Dekkers, 1991; Visscher et al., 1994 and Veerkamp et al., 2002). Economic values were estimated for milk production and reproduction traits of Holstein, and its crossbreds, with Ayrshire and Sahiwal for USA and Kenya by St-Onge et al. (2002) and Kahi and Nitter (2004). They showed that economic values for a trait were directly related to the marginal profit. Wolfová et al. (2005) estimated economic weights using a farm model based on production systems. However, economic values are scarce for cattle in the tropics (Amer et al., 1998). Defining objectives in economic terms is difficult enough in temperate agriculture, but even more so in the tropics, due to the greater environmental and managerial complexities (Franklin, 1986). Moreover, detailed economic assessments of costs (C) and revenue (R) for tropical areas, including Bangladesh are rare. Likely factors contributing to this scenario include high levels of illiteracy, poor record keeping, small herd sizes and the many different roles animals play within small-holder systems.

For BMPCUL farmer members, milk payment is on the basis of milk volume only, without any consideration of total fat and/or protein. However, in the future, the BMPCUL milk payment system could be similar to the New Zealand milk payment system (milk payment = price of fat + price of protein – milk carrier). If this takes place, the selection of dairy cattle on the basis of an index of milk yield, fat yield and protein yield will be more effective

The present study was undertaken with the objectives to (i) calculate the economic values of the traits in the breeding objectives; (ii) develop a selection index for cows (iii) estimate the genetic gain in each trait of the breeding objective, and (iv) undertake a sensitivity analysis of traits in the breeding objectives.

6.3. Methods

6.3.1. Model description and definition

In selection index theory, the aggregate genotype is generally described as a linear function of traits to be improved; each multiplied by its economic value. The economic value is the value of a unit change in the trait while maintaining the other traits in the aggregate genotype at a constant level (Hazel, 1943). In this study, a deterministic, dynamic model (Chapter 5) was used, to calculate economic values for important traits of dairy cattle under cooperative dairying in Bangladesh. The model describes quantitative relationships between average performance levels for the traits considered, and the levels of output from the farm. Total annual profit of the herd was derived from the difference between costs and revenue of the system, as shown in equation 1 below. Throughout this study all costs and prices are expressed in Bangladeshi Taka converted into US dollars (1US$ = 70 BD Taka). The productive unit is a cow within a 100-cow dairy herd and the time unit is one year. The herd dynamics are described in Chapter 5. The inputs for production were feed cost (roughage and concentrate mix was assumed at 6 taka per kg DM), and all other operational costs were considered as fixed. The input parameters were derived from Chapter 4, with the best lactation curve model (Nelder, 1966) being used to predict 270 day milk yield and these values are presented in Table 6.1. In the model presented in Chapter 5, which simulated the population dynamics, nutrition, biological and economic performance of whole farm (100 cow dairy herd) revenue was obtained from milk, beef (sale of calves, culled heifer and culled cows), draught and manure, and expenses included feed costs, health costs, reproduction costs, labour costs and marketing costs. All other operational (including those attributable to equipment, machinery and farm structures) and also management costs were considered as fixed costs. Therefore, the model reflected all the farming components. However, in the current chapter a reduced model from Chapter 5 was used, including only the revenue from the sale of milk and beef; and expenses were feed and fixed costs, which include non-feed costs (health, reproduction, management and marketing costs) per milking cow and per replacement female in age classes 1 to 3 years, respectively and all the costs were assumed to be a gross value, in calculating the individual cow income. The individual cow income was estimated after running the base model, and the economic value of each trait of interest, was obtained by rerunning the base model after changing the trait by one unit. The economic values of different traits were estimated on a per cow per year basis, reflecting effects from one year of operation. Feed is a major constraint for a dairy farm operation, and accounted for more than 60% of total costs and had a direct impact on profitable dairy farm operation. Therefore, the economic values of different traits were estimated on a per tonne of feed DM basis.

6.3.2 Returns

Under cooperative dairying in Bangladesh, milk payment is paid to the cooperative members on the basis of milk volume only, with no consideration of total fat and protein. In Chapter 5, revenue from the sale of milk, calves, heifers, and cull cows were estimated.

The following profit function of a dairy herd was used.

$$P = N_m \sum_{j=1}^{3}((CF)_i a_k Y_j) + \sum_{i=1}^{k}(S_i N_i W_i p_i) - c_m N_m - (c_{r1} N_1 + c_{r2} N_2 + c_{r3} N_3) - FC \quad (1)$$

Where: N_m, are the number of milking cows.

k is the number of age classes.

N_i is the number of animals in each age group i.

N_1, N_2 and N_3 are the numbers of animals that are 1, 2 and 3 years of age; 20% of the heifers from age class 3 are used as replacement for milking cows. Usually cows are calved at 4 years old.

S_i is the proportion of sales in each age class, i = 1 to 10 years of age and S_i = (1- survival – replacement - death).

Y_j (j = 1, 2 and 3) is the mature equivalent production (production of 6-year old cows) in kg for milk (M), fat (F) and protein (P) respectively, and a_k (k = 1, 2 and 3) is the payment price of 1 kg of M, F and P.

CF_i is a multiplicative age correction factor, relative to the production of mature cows. The assumed age adjustment factors remained the same for milk, fat and protein production and was set at 0.8, 0.95, 1.0, 1.0, 0.96, 0.92 and 0.90. (Van Arendonk, 1985 and Lopez-Villalobos, 1998).

P_i is the return per kg liveweight from the sale of animals in each age class i. W_i is the average selling weight in each age group i. The liveweight at age i in days (W_i) is calculated by using the von Bertanlanffy equation as given by Bakker and Koops (1978):

$$W_i = W_m\{1-[1-(W_0/W_m)^{1/3}]^{e\text{-}kt}\}^3$$

Where W_m = Mature liveweight (LW), W_o = Birth weight, k = constant related to rate of maturing and e = base of the natural logarithm. The ratios of birth weight and 36 months weight, to mature weight of 0.04244 and 0.5498, respectively, were used in this study.

C_m, c_{r1}, c_{r2} and c_{r3} are the variable non-feed costs per milking cow, and per replacement female in age classes 1 to 3 years respectively. Non-feed costs include health, reproduction, management and marketing costs. Non-feed costs varied between genotypes from Taka 6000 to 7500, 2500 to 3500, 3500 to 4500 and 4000 to 5500 for milking cows, one-year-old, two-year-old and three-year-old heifers, respectively.

FC is the feeding cost.

6.3.3. Energy and dry matter requirements

The energy requirements of the maintenance of individual cows, the maintenance and growth to 3 years of growing heifers, and pregnancy of individual cows, was determined by mature weight (LW), milk yield (MY), fat yield (FY) and protein yield (PY) according to AFRC (1993). The details of energy requirements are described in Chapter 5. Each calf was assumed to have consumed 20 kg DM of meal during the first 90 days of life, which was added to the total requirement of a 1 year old heifer.

For each cow, the total energy requirement (metabolisable energy (ME), per year) was the sum of ME requirement for maintenance, growth, pregnancy and production:

$$ME = ME_m + ME_g + ME_{preg} + ME_p$$

The net energy value of milk (EV_l) was predicted for each age class, using the formula of Tyrell and Reid (1965) as:

$$EV_l = 37.6F + 20.9P + 0.0948M$$

Where, M, F and P are total milk, total fat and total protein yield respectively, for each age class.

The ME requirement for lactation was determined as:

$$ME_l(MJ) = EV_l / k_l$$

Where, k_l is the efficiency for lactation (see Chapter 5). For the calculation of feed dry matter the metabolisable energy (ME) per kg of dry matter was assumed at 10 MJ/kg dry matter.

Table 6.1: Herd-level production variables assumed for the models

Variables	Genotypes				
	P	A × P	H × P	J × P	S × P
Birth wt(kg)	22[5,8]	21[3,8]	27[2]	22[8]	27[7]
Mature LW (kg)	247[1,8]	353[8]	375[6]	307[8]	307[8]
Gestation period (d)	280[4,8]	280[4,8]	278[4,8]	280[4,8]	279[1,8]
Milk production* (kg)	1697[*]	2188[*]	1993[*]	1635[*]	1823[*]
Fat production* (kg)	74[*]	77[*]	77[*]	64[*]	75[*]
Protein production* (kg)	65[*]	78[*]	66[*]	55[*]	66[*]
Calving Interval (d)	484[4]	450[4,8]	386[4,8]	390[4,8]	479[3]
Milk yield (kg/year)	1280	1775	1885	1530	1389
Fat yield (kg/year)	56	62	73	60	57
Protein yield (kg/year)	49	55	58	49	49
Calving rate	0.65[1]	0.55[5]	0.55[5]	0.52[3]	0.60[3]
Survivability up to 1 year	0.88[8]	0.84[8]	0.85[8]	0.86[8]	0.86[8]
Beef price/ liveweight (Taka)	80[8]	80[8]	80[8]	80[8]	80[8]
Price/ kg milk (Taka)	25[8]	25[8]	25[8]	25[8]	25[8]
Protein (%)	3.85	3.55	3.3	3.35	3.6

Legends: P = Pabna, H × P = Holstein × Pabna, S × P = Sahiwal × Pabna, J × P = Jersey × Pabna and A × P= Australian-Freisian-Sahiwal × Pabna.

[1]Islam et al., 2004; [2]Hirooka and Bhuiyan, 1995; [3] Nahar et al.,1992; [4] Majid et al.,1998; [5] Khan et al., 2000; [6] Ahmed and Islam,1987; [7]Islam and Bhuiyan, 1997; [8] Chapter 3; [*] Chapter 4 (from best fitted model)

6.3.4 Total herd requirements for ME

Total herd requirements for ME were calculated as:

$$ME_{herd} = \sum_{i=1}^{10} ME_{total,i} \times d_j$$

where, i = 1 to 10 years, and dj is the number of animals in each age class.

The requirements for DM were calculated by the content of ME per kg DM. It was assumed that cows were consuming roughage from Bathan (natural pastures), paddy straw, tree leaves and 2-3 kg concentrate mix per day, to fulfil their energy requirements. Requirements for DM per cow, including DM for the growing of replacements, were calculated by dividing the total requirement for DM of the whole herd by the number of cows older than 3 years.

6.3.5 Phenotypic and genotypic parameters

Heritabilities, genetic and phenotypic correlation among all traits (in the breeding objective) and characters (used as criteria) are presented in Table 6.2. Estimates of these parameters from Bangladeshi data are limited, so values from other tropical countries were included. As protein yield information was not included in any data collected from the BMPCUL, an average percentage value from the literature was used; in estimating protein yield.

6.3.6 Developing the selection index

The aggregate genotype can be written in the form:

$$H = \grave{a}Y$$

where, H is the aggregate of a genotype (expressed in $ per cow per year)

Y is a vector of genetic values for each trait (milk carrier, fat and protein yield)

and $\grave{a}$ is a vector of economic values for each trait (expressed in dollars per unit change in the mean value).

The selection index used in this study contained the variables, total fat, protein and milk yield. The selection index was developed for the selection of cows based on the mean value of first lactation records only. The index was in the form:

$$I = \grave{b} X$$

Where, X is a vector of the adjusted phenotypic values for each trait and

$\grave{b}$ is a vector of the selection index coefficients for each trait.

The selection index for this study was derived as follows:

$$\grave{b} = VY^{-1} VYG \grave{a}$$

Where, $\grave{b}$ is a vector of index coefficients

VY is a phenotypic variance-covariance matrix of characters in the index,

VYG is a genetic variance-covariance matrix between the characters in the index and the traits in the breeding objective, and

$\grave{a}$ is a vector of economic values for the traits in the breeding objectives.

Table 6.2: Heritability, repeatability, phenotypic and genotypic correlations of traits of different genotypes

Traits	Breed groups				
	P	H × P	A × P	S × P	J × P
Heritability					
MY	0.26[1]	0.28[4,8]	0.25[2]	0.26[1]	0.28[2]
FY	0.27[1]	0.30[2,1]	0.30[10]	0.27[10]	0.30[8]
PY	0.25[4]	0.26[4]	0.28[10]	0.26[1]	0.26[9]
Phenotypic Correlation					
MY & FY	0.63[6]	0.60[7]	0.69[10]	0.67[10]	0.70[7]
MY & PY	0.59[10]	0.67[3]	0.62[10]	0.59[10]	0.60[10]
FY & PY	0.79[10]	0.79[10]	0.84[10]	0.80[10]	0.72[10]
Genotypic Correlation					
MY & FY	0.57[6]	0.68[7]	0.69[10]	0.61[10]	0.69[7]
MY & PY	0.46[10]	0.48[10]	0.47[10]	0.50[10]	0.49[10]
FY & PY	0.82[10]	0.88[10]	0.78[10]	0.78[10]	0.75[10]

Legends: P = Pabna, H × P = Holstein × Pabna, S × P =Sahiwal × Pabna, J × P = Jersey × Pabna and A × P = Australian-Freisian-Sahiwal × Pabna

MY = Milk Yield, FY = Fat Yield, PY = Protein Yield.

[1]Hossain 2006; [2]Nicolas, 1995; [3]Boujenane, 2002; [4]Magofke et al., 2001; [5]Jahanshahi et al., 2002; [6]Balierio et al. 2000; [7]Banga, 1992; [8]Gogoi et al., 1992; [9]Vercesi Filho et al., 2006. [10]Assumed value.

The selection index for individual cows of different genotypes was developed with information on the milk, fat and protein yield of a 3 × 3 phenotypic variance-covariance matrix; and 3 × 3 genetic variance-covariance matrix and a vector of relative economic weights.

6.3.7 Genetic gain in individual trait in the breeding objective

The expected genetic gain per generation in the individual traits (k) of the objective in the index can be estimated as:

$$\Delta G_T = i\beta_{TI}\sigma_I$$

$$= ir_{TI}\sigma_T$$

A similar form can be used to obtain the rate of genetic gain for the individual trait:

$$\Delta G_K = i\beta_{KI}\sigma_I$$

$$= ir_{KI}\sigma_{GK}$$

$$r_{KI} = Cov(G_K, I)/(\sigma_{GK}\sigma_I)$$

therefore, $\Delta G_K = iCov(G_K, I)/\sigma_I$

where, i = selection intensity

σ_I = standard deviation of the index and

$Cov(G_{K,} I)$ is the covariance of the k^{th} trait and the index.

6.3.8 Sensitivity analysis

In the cooperative dairying system, the BMPCUL ensures regular collection of milk from their cooperative members. After collection, the raw milk is transferred to processing plants for pasteurization and packaging. The packaged milk is then sold to the distributor and the distributor sells it to the end consumer. In the processing plant of BMPCUL, besides liquid milk processing, other milk products such as butter, cheese, clarified butter, powder milk and condensed milk are also produced and sold to the market.

The farmer members of BMPCUL receive their milk payment on a liquid milk volume basis. Additional analyses were performed to test the sensitivity of economic values to changes in prices, feed cost, expenditure, milk and beef in the current payment system. Changes of ±20% with respect to the original values were considered on a per cow per year basis.

In future, the BMPCUL milk payment system could be similar to the New Zealand milk payment system (Milk payment = Price of fat + price of protein – milk carrier). The effect of paying farmers for milk solids, and penalising them for volume on selection index weightings was examined, using the current market prices in Bangladesh of butter and cheese, as surrogates for fat and protein, respectively. Sensitivity analyses using changes of ±20% in the original prices of fat + protein together were undertaken once to investigate the effects of price fluctuations on economic values.

6.4 Results

6.4.1 Costs, revenues and profit

Table 6.3 shows the costs, revenue and profit of different cattle breeds under cooperative dairying in Bangladesh on a per cow per year basis.

Table 6.3: Costs, revenues and profit from different breeds groups

Traits	Breed group				
	Pabna	H × P	S × P	J × P	A × P
DM requirement for cow (kg/year)					
Cow	2016	2651	2230	2280	2514
Replacement heifer	674	685	796	951	1222
Grand Total	2690	3336	3026	3231	3736
Price (Tk)	16140	20013	18161	19383	22414
Non feed costs					
Milking cows (Tk)	6000	7500	6500	6500	6500
Replacement Heifers (Tk)	2192	2452	2249	3248	3338
Total non-feed costs (Tk)	8192	9952	8219	9748	9838
Total expenditure (Tk)	24332	29966	26380	29132	32252
Revenue					
Milk revenue (Tk)	30066	44478	32746	35857	41751
Beef revenue (Tk)	1385	2736	926	2131	2789
Grand Total	31451	47214	33671	37988	44540
Income (Taka)	7119	51566	7291	8856	12288
Net Income, $ (1US$ = 70.00 Tk)	102	246	104	127	176

6.4.2 Economic values

The economic values for milk, fat, protein, birth weight, mature liveweight, calving interval, calving rate and survivability on a per cow per year and a per tonne of feed dry matter (DM) basis for different genotypes of dairy cows are presented in Tables 6.4 and 6.5, respectively.

For both on a per cow and on a per tonne of feed DM basis the economic values of milk yield and survivability were positive, while the values for fat, protein, calving interval, calving rate, mature liveweight, and birth weight were negative. On a per cow basis, economic values for milk yield, fat yield and protein yield were the same across genotypes. Overall, the economic values were relatively similar across all the genotypes. Economic values are more positive or more negative on per cow basis compared with per tonne of feed DM.

Table 6.4: Economic values (US$ per unit) for different genotypes on the basis of per tonne feed dry matter

Traits	Genotypes				
	P	H × P	S × P	J × P	A × P
Milk yield	0.12	0.09	0.11	0.09	0.09
Fat yield	-0.29	-0.27	-0.23	-0.22	-0.19
Protein yield	-0.16	-0.15	-0.13	-0.12	-0.10
Liveweight	-0.23	-0.16	-0.18	-0.16	-0.14
Birth weight	-0.03	-0.12	-0.08	-0.15	-0.18
Calving interval	-0.28	-0.36	-0.26	-0.32	-0.26
Survivability	0.43	0.44	0.39	0.51	0.23
Calving rate	-0.25	-0.24	-0.25	-0.23	-0.19

Legends: H = Holstein-Friesian, P = Pabna, S = Sahiwal, J = Jersey and A = Australian-Friesian-Sahiwal

Table 6.5: Economic values (US$ per unit) for different genotypes on a per cow basis

Traits	Breed group				
	P	H × P	S × P	J × P	A × P
Milk yield	0.32	0.32	0.32	0.32	0.32
Fat yield	-0.52	-0.52	-0.52	-0.52	-0.52
Protein yield	-0.29	-0.29	-0.29	-0.29	-0.29
Liveweight	-0.39	-0.27	-0.39	-0.37	-0.37
Birth weight	-0.05	-0.23	-0.17	-0.35	-0.49
Calving interval	-0.79	-1.32	-0.82	-1.08	-0.99
Survivability	0.88	1.03	0.96	1.35	0.50
Calving rate	-0.51	-0.54	-0.59	-0.59	-0.63

Legends: H = Holstein-Friesian, P = Pabna, S = Sahiwal, J = Jersey and A = Australian-Friesian-Sahiwal

The economic values for traits in the selection objective for 5 different genotypes based on a possible future milk payment of fat + protein – milk carrier on a per cow per year basis are presented in Table 6.6. Economic values of milk carrier (-US$0.05) to be similar for all the genotypes but the economic values of fat, protein, liveweight and calving interval varied.

Table 6.6: Economic values (US$ per unit) for different genotypes on a per cow basis when milk payment is based on the value of fat and protein yield and with a penalty for milk volume

Traits	Breed group				
	P	H × P	S × P	J × P	A × P
Milk yield	-0.05	-0.05	0.05	-0.05	0.05
Fat yield	3.24	3.26	3.25	3.23	3.34
Protein yield	5.35	5.65	5.63	5.6	5.68
Liveweight	0.-40	-0.27	-0.40	-0.37	-0.27
Calving interval	-0.82	-1.21	-0.81	-0.99	-0.98

Legends: H = Holstein-Friesian, P = Pabna, S = Sahiwal, J = Jersey and A = Australian-Friesian-Sahiwal

6.4.3 Selection index and genetic gain per cow

The index weighting factors for total milk, fat and protein yields and the selection index values, which is the average value of an animals adjusted phonotypic (mean) value of different genotypes, are presented in Table 6.7. Milk volume has positive index weightings for all genotypes, while protein yield has only negative values. The Pabna, Sahiwal × Pabna and Jersey × Pabna genotypes have negative index weightings for fat yield, while the Holstein x Pabna and Australian-Friesian-Sahiwal genotypes have positive values.

The predicted rates of genetic changes in milk yield, fat yield and protein yield when selection is based on farm profit are shown in Table 6.6. Milk yields show positive predicted responses for all genotypes with the responses for Pabna cattle, Holstein × Pabna and Sahiwal × Pabna being similar and the highest, while Jersey × Pabna and Australian-Friesian -Sahiwal × Pabna were similar and also the lowest. Predicted responses for protein yield were negative for all genotypes with Pabna cattle, Holstein × Pabna and Australian-Friesian -Sahiwal × Pabna being similar and the Sahiwal × Pabna and Jersey × Pabna being lowest. Responses to selection for fat yield were positive in Holstein × Pabna and Australian-Friesian -Sahiwal × Pabna cattle, but negative for the other genotypes.

Table 6.7: Index weighting factors, index values and genetic gains (per i) for individual traits of the breeding objective for different genotypes

Items	Genotypes				
	Pabna	H × P	S × P	J × P	A × P
Weighting factors					
Milk	0.09	0.09	0.10	0.10	0.08
Fat	-0.05	0.50	-0.23	-0.014	0.58
Protein	-0.41	-0.83	-0.23	-0.37	-1.15
Index value					
US$	157.74	173.04	141.56	156.73	222.19
Genetic gain per generation					
Milk	49.65i	47.65i	46.96i	21.02i	27.10i
Fat	-0.76i	12.22i	-4.12i	-0.17i	8.32i
Protein	-4.15i	-6.75i	-0.04	-2.64i	-6.50i

Legends: H = Holstein-Friesian, P = Pabna, S = Sahiwal, J = Jersey and A = Australian-Friesian -Sahiwal.

6.4.7 Sensitivity analysis

Table 6.8 shows the economic values for traits in the selection objective when payment is for milk volume for 5 genotypes, after changing price levels by ±20% for various income and cost traits on a per cow per year basis. The economic values for traits in the selection objective for 5 different genotypes, based on a possible future milk payment of fat + protein – milk carrier with changes of ±20% price levels of fat + protein together on a per cow per year basis, are presented in Table 6.9.

Table 6.8: Sensitivity analysis of economic values for milk production and reproduction traits in different genotypes on per cow basis when the milk payment to farmers is on milk volume only

Input/ Output	Price level (%)	P								H × P								S × P							
		MY	FY	PY	LWt	CI	CR	SUR	Profit (US$)	MY	FY	PY	LWt	CI	CR	SUR	Profit (US$)	MY	FY	PY	LWt	CI	CR	SUR	Profit (US$)
Base		0.32	-0.52	-0.29	-0.39	-0.79	-0.51	0.88	101.7	0.32	-0.52	-0.29	-0.27	-1.23	-0.54	1.03	246.4	0.32	-0.52	-0.29	-0.39	-0.82	-0.59	0.96	104.2
Feed	+20	0.32	-0.62	-0.35	-0.48	-0.77	-0.58	1.03	55.6	0.32	-0.62	-0.35	-0..35	-1.28	-0.61	1.12	189.8	0.32	-0.62	-0.35	-0.49	-0.80	-0.66	1.15	44.6
	-20	0.33	-0.42	-0.23	-0.29	-0.82	-0.44	0.78	147.8	0.33	-0.42	-0.23	-0.20	-1.36	-0.47	0.85	304.0	0.33	-0.42	-0.23	-0.31	-0.85	-0.83	0.52	148.8
Milk	+20	0.39	-0.52	-0.29	-0.39	-0.82	-0.51	0.90	187.7	0.39	-0.52	-0.29	-0.27	-1.63	-0.54	0.99	373.9	0.39	-0.52	-0.29	-0.40	-1.01	-0.58	0.99	190.1
	-20	0.26	-0.52	-0.29	-0.39	-0.75	-0.51	0.90	15.8	0.26	-0.52	-0.29	-0.27	-1.12	-0.54	0.99	119.8	0.26	-0.52	-0.29	-0.40	-0.63	-0.58	0.99	29
Beef	+20	0.31	-0.52	-0.29	-0.37	-0.75	-0.50	0.89	105.7	0.32	-0.52	-0.29	-0.25	-1.32	-0.53	0.97	254.7	0.26	-0.52	-0.29	-0.39	-0.63	-0.58	0.96	99.17
	-20	0.31	-0.52	-0.29	-0.40	-0.75	-0.51	0.92	97.7	0.32	-0.52	-0.29	-0.29	-1.32	-0.53	1.01	239.1	0.26	-0.52	-0.29	-0.41	-0.63	-0.58	1.02	93.88
Expendi	+20	0.31	-0.52	-0.29	-0.40	-0.75	-0.51	0.90	78.3	0.32	-0.52	-0.29	-0.27	-1.32	-0.58	1.07	218.5	0.26	-0.52	-0.29	-0.40	-0.63	-0.61	1.06	71.54
ture	-20	0.31	-0.52	-0.29	-0.40	-0.75	-0.47	0.84	125.1	0.32	-0.52	-0.29	-0.27	-1.32	-0.51	0.91	275.4	0.26	-0.52	-0.29	-0.40	-0.63	-0.55	0.92	121.51

Table 6.8 (continued)

Input/ Output	Price level (%)	J × P								A × P							
		MY	FY	PY	LWt	CI	CR	SUR	Profit (US$)	MY	FY	PY	LWt	CI	CR	SUR	Profit (US$)
Base		0.32	-0.52	-0.29	-0.37	-1.08	-0.59	1.35	126.5	0.32	-0.52	-0.29	-0.37	-0.99	-0.63	0.50	175.6
Feed	+20	0.32	-0.62	-0.35	-0.46	-1.04	-0.69	1.59	71.1	0.32	-0.62	-0.35	-0.46	-1.51	-0.63	0.89	111.3
	-20	0.32	-0.42	-0.23	-0.28	-1.11	-0.52	1.22	181.9	0.33	-0.52	-0.29	-0.27	-1.03	-0.46	0.40	239.3
Milk	+20	0.39	-0.52	-0.29	-0.37	-1.32	-0.61	1.41	228.9	0.39	-0.52	-0.29	-0.27	-1.26	-0.54	0.85	294.6
	-20	0.26	-0.52	-0.29	-0.37	-0.88	-0.61	1.41	24.1	0.26	-0.52	-0.29	-0.27	-0.80	-0.54	0.85	56.1
Beef	+20	0.32	-0.52	-0.29	-0.35	-1.08	-0.61	1.39	132.6	0.33	-0.52	-0.29	-0.34	-1.03	-0.53	0.62	183.3
	-20	0.32	-0.52	-0.29	-0.39	-1.08	-0.61	1.42	120.4	0.33	-0.52	-0.29	-0.39	-1.03	-0.55	0.67	167.3
Expenditure	+20	0.32	-0.52	-0.29	-0.37	-1.36	-0.64	1.48	100.3	0.33	-0.52	-0.29	-0.27	-1.03	-0.57	0.78	139.5
	-20	0.32	-0.52	-0.29	-0.37	-1.36	-0.56	1.30	154.3	0.33	-0.52	-0.29	-0.27	-1.03	-0.52	0.56	147.6

Legends: P = Pabna, H = Holstein, S = Sahiwal, J = Jersey, A = Australian-Friesian-Sahiwal

MY = Milk Yield, FY = Fat Yield, PY = Protein Yield, LWt = LiveWeight, CI = Calving Interval, CR = Calving Rate, SUR = Survivability

Table 6.9: Sensitivity analysis with changes of ±20% price levels of fat + protein together of economic values for milk production and reproduction traits in different genotypes on per cow basis when the milk payment is based on the value of fat and protein and with a penalty for milk volume

Price level	P						H × P						S × P					
	Milk	Fat	Protein	Live wt	CI	Profit (US$)	Milk	Fat	Protein	Live wt	CI	Profit (US$)	Milk	Fat	Protein	Live wt	CI	Profit (US$)
Base	-0.05	3.24	5.35	-0.40	-0.82	126.0	-0.05	3.26	5.65	-0.27	-1.21	170.27	-0.05	3.25	5.63	-0.40	-0.81	110.4
+20	-0.06	3.99	6.80	-0.40	-1.01	217.9	-0.06	4.01	6.83	-0.27	-1.50	279.50	-0.06	4.01	6.82	-0.40	-0.99	200.4
-20	-0.05	2.49	4.44	-0.40	-0.63	34.1	-0.05	2.50	4.36	-0.27	-0.93	61.04	-0.05	2.50	4.45	-0.40	-0.62	20.4

Continuation of Table 6.9

Price level	J × P						A × P					
	MY	FY	PY	LWt	CI	Profit (US$)	MY	FY	PY	LWt	CI	Profit (US$)
Base	-0.05	3.23	5.60	-0.37	-0.99	104.67	-0.05	3.34	5.68	-0.27	-0.98	179.78
+20	-0.06	3.98	6.78	-0.37	-1.22	201.86	-0.06	4.10	6.87	-0.27	-1.20	278.20
-20	-0.05	2.48	4.42	-0.37	-0.76	14.27	-0.04	2.60	4.50	-0.27	-0.76	79.36

Legends: P = Pabna, H = Holstein, S = Sahiwal, J = Jersey, A = Australian-Friesian-Sahiwal.

MY = Milk Yield, FY = Fat Yield, PY = Protein Yield, LWt = LiveWeight, CI = Calving Interval

6.5 Discussion

The aim of this study was to estimate economic values, index weighing factors, rates of genetic gain, and sensitivity to changes in expenses and income on the basis of profit per cow per year for traits included in a breeding programme for cooperative dairying in Bangladesh.

6.5.1 Costs, revenues and profit

In the model of Chapter 5, income was obtained from milk, beef, draught and manure, and the expenses included feed costs, health costs, reproduction costs, labour costs, marketing costs and all other operational such those attributable to equipment, mechinary and farm stuctures and management costs as fixed costs. However, in the current model, income was derived from the sale of milk and beef; and costs included only feed and fixed costs, which include non-feed costs (health, reproduction, management and marketing costs) per milking cow and per replacement female in age classes 1 to 3 years, respectively. The net annual incomes for Pabna cattle, Holstein × Pabna, Sahiwal × Pabna, Jersey × Pabna and Australian-Freisian-Sahiwal × Pabna differed between the two models. The Hostein × Pabna have higher profitability in Table 6.3 than in Table 5.4, while all other genotypes show lower profits. This is because of the differences in derivation of profits between the two models. The milk production of Hostein × Pabna cows was higher than other genotypes, which was reflected in greater profit than the other genotypes in the model were payment was solely on milk volume. The impact of different models on profitability have been illustrated by many researchers (e.g. Ponzoni and Newman, 1989).

6.5.2 Economic values for milk production and reproduction traits

Economic values of total milk yields were positive for all the genotypes per cow per year and also on a per ton of feed DM basis. Positive economic values for milk yield are expected, as payment to farmers is on milk volume only. In the current milk payment system used by BMPCUL, farmer members’ are paid on the basis of milk volume with no consideration of fat and protein yield. Positive economic values for milk yield were also reported by Kahi et al. (2004) in the pasture based system of Kenya, but elsewhere in the literature, economic values for milk yield were normally negative (Beard, 1988; Dekkers, 1991; Bekman and Van Arendonk, 1993; Gibson, 1989; Groen, 1989; Veerkamp et al., 2002 and Lopez-Villalobos et al., 2005). However, in these studies, farmers were paid on the total fat and protein yield, minus the cost associated with milk volume.

The negative economic values for fat and protein were of the same magnitude for all genotypes on per cow per year basis. However, they differed between genotypes on a per ton of feed DM basis, due to the different feed requirements of different sized cows. The economic value of protein was half as negative as fat, on a per cow per year and per tonne of feed DM. This is primarily due to be almost double quantity of energy required to produce 1kg of protein (20.9MJ) versus 1kg of fat (37.6MJ). These negative economic values for fat and protein yield were anticipated, due to the current milk payment system in Bangladesh. Positive economic values for fat and protein where payment of milk is based on price of fat and protein was reported by Beard (1988); Bekman and Van Arendonk (1993); Gibson (1989); Groen (1989); Pieters et al. (1997); Visscher et al. (1994), Lopez- Villalobos et al. (2005).

Economic values for a one day increase in calving intervals ranged from -US$1.32 to -US$ 0.79 and –US$0.36 to –US$0.26 per cow per year and per tonne of feed DM basis. This is anticipated, because the reduction of calving intervals improves farm profit, through higher milk yields. Longer calving intervals are more significant when the milk output is fixed. Veerkamp et al. (2002) also found negative economic values for calving intervals, but Kahi et al. (2004), derived a positive economic value for calving intervals, as they used milk yield (already adjusted to the calving interval) as an input parameter rather than lactation milk yield in their model. They derived economic value for calving intervals by changing the one unit genetic merit of calving interval, allowing no simultaneous change in genetic merit of milk yield. This change resulted in less milk per time unit and an increasing calving interval, is expected to generate a negative economic value of calving interval, but was not handled by the model.

Economic values for calving rate were negative for all genotypes. The negative values of calving rate were attributed due to the estimation of economic values based on a one-year-farming operation. The higher calving rate increased the number of one-year-old calves in the herd. These calves contributed beef income, but no milk income, as only 4^+ year-old-cows produce milk. However, the calves' feeding and management costs were added to the expenditure for a one-year operation, and the beef income was lower than the total of these costs. These negative values reflect reduced income from the sale of animals for beef. In addition, an increased number of replacement heifers were needed, further reducing numbers of animals available for sale (although sales from cull cows might increase).

6.5.3 Economic values for mature liveweight and birth weight

Economic values of mature liveweight, for different genotypes, ranged from -US$ 0.39 to -US$ 0.27 to and -US$0.23 to -US$0.14 on per cow and per tonne of feed DM basis, respectively. Similar findings have been reported by several workers (Visscher et al., 1994; MacNeil et al., 1994; LIC, 2000 and Lopez-Villalobos et al., 2005). Economic values for mature liveweight were negative, as a larger cow requires more energy for the maintenance of its weight, and that energy is unavailable for production purposes. The relative importance of (mature) liveweight, to the profit of a dairy cow/farm has been examined by Morris and Wilton (1977); Goddard (1985); and Ahlborn and Dempfle (1992) but other than in New Zealand, this trait is usually ignored in applied breeding programmes for dairy cattle. The inclusion of feed intake/feed efficiency in selection objectives (with liveweight as the selection criterion) will not necessarily cause mature weight to decrease but, given a positive genetic correlation between weight and milk production, it might prevent liveweight from increasing. Differences between the genotypes were found. Generally, the heavy (Holstein × Pabna) liveweight cows have the least negative (-0.27) economic value with the other genotypes being about the same (-0.37 to -0.39). The liveweight for lactating cows have to be accounted for. The Holstein × Pabna produces least milk yield per kg liveweight (5.3kg/kg livewith) than other genotypes while Pabna cattle produces highest (6.9 kg/kg liveweight) and others produces intermediate.

Economic values for birth weight were also negative, ranging from -US$0.48 to -US$0.05 per kg per animal per year. This is in contrast to the positive values reported by Groen (1989a). Birth weight is used in the equations to predict weights at different ages and therefore is associated with feed requirements. Birth weight is positively correlated with weight at sale and hence beef production, and the growth of replacement heifers and hence sale value, which would suggest a positive economic value. The negative economic value of birth weight would suggest that the increased beef production and improved replacement heifer values did not offset feed costs for producing a kg of weight gain.

6.5.4 Economic values for survivability

Economic values of different genotypes for survivability were positive for all the genotypes. The Jersey × Pabna cattle obtained the highest (US$1.35 per cow per year, US$0.52 per ton of feed DM basis) and Australian-Friesian-Sahiwal × Pabna genotype has the lowest (US$0.50 per cow per year and US$0.23 per tonne of feed DM basis) with the other three genotypes being intermediate. The differences of survivability were attributed to the breed differences, mean (prdoction) levels and also to the differences of costs and return of the particular breed using in the model. Differences due to genotype × environment interactions were reported by Kahi et al. (2004). Various authors (e.g. Burnside et al., 1984; Visscher et al., 1994; Veerkamp et al., 1995) have used different approaches in estimating the economic value of herd life (or related traits) and all reported positive economic values. An increase in survival reduces the number of herd replacements needed each year, leaving more animals to sell and, thereby increasing income. In addition, there will be more mature cows in the herd, raising milk output. The underlying causes of survivability are disease resistance, nutritional status and other stresses and these are important in cooperative dairying in Bangladesh

6.5.5 Economic values for different traits when milk payment is based on milk, fat and protein value

The economic values for the traits studied were similar to those reported by Beard (1988); Visscher et al. (1994); Veerkamp et al. (2002) and Lopez-Villalobos et al. (2006) in temperate conditions. Milk yield had a negative economic value while protein yield had an economic value about twice that of fat yield in all genotypes. The economic value of fat was higher in Australian-Friesian-Sahiwal × Pabna (US$3.34) than other genotypes whose values ranged between US$ 3.23 and US$3.25. The economic value of protein was lower in Pabna cattle than in all other genotypes. These differences were occurs with the breed and production level differences of individual cows and also the differences of costs ane return in the current model.

6.5.6 Selection index and genetic gain

The index weightings for milk yield were positive for all genotypes but were negative for protein yield. Index weightings for fat yields were positive for Holstein × Pabna and Australian-Friesian-Sahiwal × Pabna but were negative for other genotypes. This positive index weighting for fat yield for these two genotypes was attributed for the effects of phenotypic and genotypic correlations and (co)variances of milk and fat yield, and also to the effects of the current milk payment system. The effect of phenotypic variance and covariance ratios on index weightings, has been reported by many researchers (e.g. Hazel, 1943; Hazel et al., 1994; Hohenboken, 1985 and Falconer, 1990). Beard (1988) reported positive index weights for fat and protein and negative for milk carrier, which was attributed to the milk payment systems. Different index values for different breeds were observed, which attributed with the differences of index weightings and mean phenotypic yield differences of breeds. Many researchers (e.g. Weller, 1994 and Hazel et al.,1994) reported similar causes for the differences of the index value. This higher index value of Australian-Friesian-Sahiwal × Pabna genotype reflects that the influence of milk weighting factors is more important for this genotype than other genotypes, because in the current milk payment system, the farmers are paid on the basis of milk volume, and not on a total fat and/or protein basis. Kahi and Nitter (2004) reported similar results on the pasture based production system in Kenya. When the population is selected on the basis of milk yield, the rate of genetic progress is positive and it differs significantly in breed differences. However, when payment is on milk solids the weighting for fat and protein yield are positive, although such values would be inadvisable under the current milk payment system because milk yield has a positive effect on the profitability of the farm.

6.5.7 Sensitivity analysis

Changes in milk prices by ±20% did not change within breed the economic values of fat yield, protein yield, liveweight, calving rate and survival. However, the economic value for milk volume increased with the increase in milk value, while the economic value for calving interval became increasingly negative, with an increase in milk price. The high sensitivity of economic values to the price of milk was anticipated as a high percentage of revenue comes from milk sales. A similar finding was reported by Kahi and Nitter (2004) from pasture based dairy production systems in Kenya. The more negative economic values of calving interval arose from the effects of the estimated of yearly yields of milk, fat and protein from the total yield per calving interval. The sensitivity of economic values for liveweight, calving interval, calving rate and survivability, differed between genotypes after changing the milk price by ±20%. Furthermore, the economic values of all traits differed between the genotypes except for fat and protein yield. Lower economic values for milk yield and liveweight were obtained for Sahiwal × Pabna and calving interval for Holstein × Pabna than for other genotypes. The economic value of calving rate was higher (less negative) for this genotype. This was attributed to the number of cows required in each herd for the derivation of economic values.

Changing feed costs by ±20% did not greatly affect the economic values for milk volume and calving interval, however, economic values for all other traits were changed. Higher feed prices caused more negative economic values for fat, protein yield and liveweight. This is because of the energetic cost of producing fat and protein and maintaining liveweight, which does not generate any additional revenue. The sensitivity of the economic values was similar for all genotypes. Visscher et al. (1994) showed how economic values of fat and protein, and milk carrier changed with the change of scenarios for a pasture-based dairy production system in Australia. The economic values for calving rate became negative but were positive for survival, as feed price increased, in all genotypes. The negative economic value of calving rate was attributed to the increased number of one-year-old calves in the herd, but these calves did not contribute more milk income relative to beef income. Moreover, calf feeding and management costs were incurred in a one-year operation, but the resulting beef income was lower than the costs.

Changing the beef prices by ±20% had little/no effect on economic values of all traits except liveweight for all genotypes. Beef contributes little to income due to the small number of animals in the herd. The beef price was influenced by the number of cows in the herd and also the culling percentages. Changes of economic weights can be produced by increasing or decreasing cow numbers from herd (Smith et al., 1986).

When payment is based on fat+protein-milk carrier the economic values of milk, fat, protein yield and calving interval (Table 6.9) were sensitive to ±20% fluctuations of market prices of milk, fat and protein. High sensitivity of economic values for the price of milk, fat and protein yield was anticipated because a high percentage of revenue comes from the total milk solids yield. Similar results were reported by Kahi et al. (2000) in pasture based production system in Kenya. In that sensitivity analysis, the economic values of liveweight were not sensitive to changes of the milk, fat and protein. This may be a function of the milk payment system, which does not consider milk, fat and protein yield basis on a liveweight basis.

Feed is a major expense in all dairy producing operations, and it significantly influences the profitability of a dairy farm. In Bangladesh, concentrates are expensive; therefore, their use is limited. However farmers rearing temperate breeds and their crossbreds, do feed their cows concentrate mix. Due to the shortage of land, and also capital, acess to pasture is very limited. In the BMPCUL areas during the wet season, all breeds and age groups are kept in unplanned semi-intensive housing, where they are fed mainly paddy straw. In the dry season, animals are grazed on pasture land, popularly known as Bathan. Throughout the year lactating cows are fed 2-3 kg/day/cow of concentrates. Therefore, the breeding of animals can efficiently utilise this feeding system, especially in the smallholder dairy sector. Most of the semen entering the country originates from countries where no emphasis is placed on the ability to utilise tropical pastures or on the adaptation to the other tropical stresses that prevail. In addition, more emphasis is placed on yields of fat and protein, than on milk volume. In Bangladesh, the payment of milk is based on milk volume, and this is not expected to change in the near future. The economic values of fat and protein yield are negative and their inclusion in the genetic improvement should be limited under the current milk payment system. For a genetic improvement programme, the selection of dairy cattle on the basis of milk, fat and protein yield may be incorporated in the future, and then the New Zealand milk payment system (Milk payment = Price of fat + price of protein – milk carrier) could be adapted for implementation under cooperative dairying in Bangladesh.

6.6. Summary

A deterministic model was developed based on the relationship between average performance levels for the traits of breeding objectives and level of output on a 100 cow dairy herd consisting of five different genotypes (Pabna, Australian-Friesian-Sahiwal × Pabna, Holstein × Pabna, Jersey × Pabna and Sahiwal × Pabna) under cooperative dairying conditions in Bangladesh.

The total annual profit of the individual cows was derived from the difference between costs and revenue and the economic values of each trait in the breeding objectives were estimated rerunning the model after changing the trait value by one unit. A sensitivity analyses was carried out with changes the base price of feed, milk, beef and fixed costs by ±20%. The annual profit per cow per year, was highest for Holstein × Pabna and lowest for Pabna. Similar economic weights of milk yields for various genotypes on a per cow per year basis were observed but for fat and protein were the negative economic values, which due to there being no payment to farmers for the fat and/or protein yield. Economic values for mature liveweight, birth weight, calving interval and calving rate were negative for all genotypes but the economic value for survivability was positive all the genotypes. The sensitivity analysis indicated that the economic values for responsive traits (milk yield, calving interval, survival, and liveweight) might change depending on the level of input and output prices. Economic values for traits in the breeding objective reflect how the traits impact on farm profit.

The index values and genetic gains of individual trait indicate that the selection of cows on the basis of milk volume would be more practical in Bangladesh than total fat and protein yields, as this would have a positive impact on profits with the milk payment system which is in use today.

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CHAPTER SEVEN

Multitrait Simulation Modelling for the Dairy Cattle Improvement under Cooperative Dairying Conditions in Bangladesh

7.1 Abstract

In this simulation study, individual cow performance for yields of milk, fat and protein, liveweight and longevity were simulated by using a stochastic statistical model. Additive genetic effects, permanent and temporary environmental effects, herd and age effects were included in the model, along with Mendelian sampling and consideration of inbreeding effects. A total of 10,000 Pabna cows were simulated and they were distributed in 200 herds with herd size ranging from 40 to 60 milking cows. The herds were bred for 20 years assuming either progeny, or parent average selection schemes. All animals were ranked on the basis of an economic selection index. Selection of replacement cow and breeding bulls was based on one of three selection objectives: genetic merit for milk merit, genetic merit for milk and survivability or total genetic merit which included milk yield, fat yield, protein yield, liveweight and longevity. In each year, 150 cows with the best predicted genetic merit were selected for the production of breeding bull and cow replacements. Selection of new bull and cow replacements based on pedigree information showed higher genetic gains than the progeny testing breeding schemes for all the traits. This was due to the differences in generation interval, and accuracy of the two selection schemes, in addition to the size of the progeny group which also impacted on genetic gains. The highest genetic gain (US$15.03/year) was obtained when the selection objective was for milk yield genetic merit compared with (US$10.95/year) when the selection was on total genetic merit. The genetic trends of both cows and breeding bulls, showed that increased genetic gain over years was mainly dependent on selection of bulls and cows that were mated as parents. This simulation model offers breeding companies an opportunity to compare different selection objectives, and to evaluate different breeding schemes and correlated responses of the various traits. The use of this simulation model for the dairy cattle improvement in Bangladesh will assist in meeting the national demand of milk.

(Key words: multitraits, stochastic simulation model, breeding schemes and selection objective)

7.2 Introduction

The breeding objective is a statement of the economic worth of an animal from a genetic perspective (Harris et al, 1984; Harris and Newman, 1994), which can be defined as the combination of economically important traits to be improved to achieve the breeding goal. After setting the breeding objective it is important to decide which traits can be used to select individuals for breeding, these traits being known as selection criteria. There are two steps involved in the development of the selection objective, step 1: to identify the traits that affects profitability and step 2: to define the economic values of the traits. A selection objective allows animals to be ranked with a single value, termed the aggregate economic value or index value, which balance the good and poor attributes of each individual. This index can be termed the total merit and is calculated as the sum of the breeding values for each trait each weighted by its economic value. Miglior et al. (2005) found that a total economic merit index provided greater economic returns for animal evaluation, than a single trait merit index.

There are some traits such as fertility, longevity and resistance to diseases that are important for the genetic evaluation of cows and young bulls, but estimations of the breeding values (EBV) of these traits have less accuracy due to low heritabilities. Among these traits, longevity or productive life is an important trait, which affects dairy farm profitability. Increasing longevity reduces replacement cost, changes herd age structures allowing a higher proportion of older cows and allows for increased culling for milk production (Madgwick and Goddard, 1989).

More rapid genetic gains are possible if superior sires are selected and kept for breeding purpose. The sires can be selected on the basis of their dams and/or progeny performance. Rendel and Roberson (1950) developed the four pathways model (dams to breed dams, dams to breed sires, sires to breed dams and sires to breed sires) to describe the selection of sires and dams as parents for the generation of bull and cow replacements.

At present there are no systematic dairy cattle genetic improvement programmes operating under the Bangladesh Milk Producers' Cooperative Union Limited (BMPCUL) due to constraints such as small herd size, lack of logistical, financial and infrastructure support and inadequate information on different traits and current market values of different items. This means that experimental analysis using industry herd information is difficult and largely unachievable. Therefore, the use of stochastic computer simulation models is helpful in examining potential genetic improvement programmes for possible future use (Sørensen et al., 1992).

In order to introduce a genetic improvement programme under BPMCUL in the future, the present study was undertaken with the following objectives (i) to develop a multitrait simulation model using a stochastic approach, (ii) to evaluate two breeding schemes with three different selection objectives considering milk yield, fat yield, protein yield, liveweight and longevity over 20 years of selection and mating, (iii) to compare the genetic gains derived from stochastic and deterministic approaches and (iv) to study the correlated responses on longevity with other traits (milk yield, fat yield, protein yield and liveweight).

7.3 Materials and methods

7.3.1 Simulation of breeding values and phenotypic observations

In this simulation study, Pabna cattle were considered as a model breed under Bangladesh Milk Producers' Cooperative Union Limited (BMPCUL). This breed is more adapted and feed efficient than temperate breeds and crossbreds and will be more suitable for milk production under small-holder farming in Bangladesh. The three selection objectives, milk production, milk and survivability, and total merit, were set under two selection schemes. Traits considered as the selection criteria were milk yield, fat yield, protein yield, liveweight and longevity. These traits were considered as they are heritable, correlated and easily measurable, and were adjustable for measurable environmental variation. Genetic parameters were obtained from the literature and their genetic (co)variance matrix was positive definite. The trait longevity and survivability are different but the survival is the underlining cause of longevity and more related therefore, the economic value of survivability of Table 6.5 was used as the economic value of longevity in this study. A detailed description of the economic values of these traits was shown in Chapter 6. The sires and cows to be parents of the next generation were selected on a total index, which gave appropriate weights to five traits.

The methodology used in developing the genetic simulation model is based on principles and models of Middleton (1982), Tier (1984) and Falconer and Mackay (1997). Five traits (milk yield, fat yield, protein yield, liveweight and longevity) of dairy cows were simulated over 20 years with the following model:

$$Y_{ijkn} = \mu + H_i + A_j + G_n + P_n + E_{ijkn}$$

where, Y_{ijkn} is the phenotypic value of each of the traits

μ is the overall mean of the population

H_i is the effect of herd

A_j is the effect of age

G_n is the additive genetic effect

P_n is the permanent environmental effect and

E_{ijkn} is the temporary effect

The effects of dominance and epistasis were not modelled in this simulation.

A total of 200 herds, each with a herd size ranging from 40 to 60 cows and age structures from 4 to 10 years, were simulated. Levels of production were assumed under cooperative dairying conditions of Bangladesh. Phenotypic standard deviations, economic weights and age effects are listed in Table 7.1. The (co)variance matrices of herd effects, additive genetic values, permanent and temporary environmental effects were calculated from the parameters given in Table 7.1 and 7.2.

The herd effects were assumed to be 10-15% of the variation from the phenotypic standard deviations. The vector of herd effects (H_i) of the traits were generated as the product of a Cholesky decomposition matrix of herd effect (co)variance matrix (HD), and a vector of randomly selected pseudo-normal deviates (Φ_i). The H_i vector was generated as:

$$H_i = HD * \Phi_i$$

The age effect was assumed from the mean deviation and was set to 0 for age year 6 and 7. No age adjustments were considered for longevity, therefore cows remained in the herd according to their higher breeding value for longevity. All other age groups were assumed to perform more poorly than the 6 and 7 year old cows (Table 7.1). The age effect was added to each trait along with the effects of herd, additive genetic and environmental effects.

The genotypic variance (σ^2_G) of the base cows was calculated as follows:

$$\sigma^2_G = h^2 \sigma^2_p$$

Where, h^2= heritability of the traits and

σ^2_p = phenotypic variance for the traits.

A vector of additive Genetic values (Gn) for all the traits were generated as the product of a Cholesky decomposition matrix of genetic (co)variance matrix (AD) and a vector of randomly selected pseudo-normal deviates (Φ_i). The Gn was generated as:

$$Gn = AD * \Phi_i$$

Table 7.1: Simulated traits, their means, standard deviations, economic values and age effects

Traits	Average	Phenotypic standard deviation (kg)	Economic values(US$ per unit)	Age effects						
				10 year	9 year	8 year	7 year	6 year	5 year	4 year
Milk yield (kg)	1697.4	262.50	0.32	-128	-102	-51	0	0	-64	-256
Fat yield (kg)	77.7	9.10	-0.52	-6.03	-4.83	-2.41	0	0	-3.21	-12.07
Protein yield (kg)	71.4	8.70	-0.29	-5.43	-4.34	-2.20	0	0	-2.72	-10.86
Liveweight (kg)	259.4	16.40	-0.39	-11.31	-2.49	-4.41	0	0	-18.69	-30.57
Longevity (d)	2752	129.30	0.88	0	0	0	0	0	0	0

The breeding value of the progeny was simulated as follows:

$$G_I = 0.5 G_S + 0.5 G_D + \sqrt{1/2} . * (1 - (F_{i(Sire)} + F_{i(Dam)})/2 * M$$

where, G_S and G_D are the breeding values of the sire and dam, respectively, $F_{i(Sire)}$ and $F_{i(Dam)}$ is the coefficient of inbreeding of sire and dam, respectively and M is the Mendelian sampling deviation as shown below.

$$M = MD*\Phi_i$$

Where, MD is the Cholesky decomposition matrix of genetic (co)variance matrix, which was calculated in consideration of Mendelian sampling and Φ_i is a vector of randomly selected pseudo-normal deviates.

Temporary Environmental variance (σ^2_E) was calculated as:

$$\sigma^2_E = (1 - r) * \sigma^2_p$$

where, r = repeatability of the traits and

σ^2_p = phenotypic variance for the traits.

Permanent Environmental variance (σ^2_n) was calculated as:

$$\sigma^2_n = (r - h^2) * \sigma^2_p$$

where, r = repeatability of the traits

h^2= heritability of the traits and

σ^2_p = phenotypic variance for the traits.

Environmental correlation between traits X and Y was computed as:

$$r_E = (r_p - h_X h_Y r_G)/[(1 - h^2_X) * (1 - h^2_Y)]^{1/2}$$

where, r_P is the phenotypic correlation between traits X and Y;

r_G is the genetic correlation between traits X and Y; and

h_X and h_Y are the square roots of heritabilities for traits X and Y, respectively.

The vector of environmental effects (E) for the i^{th} trait were generated as the product of a Cholesky decomposition matrix of environmental variance covariance matrix

(ED) and a vector of randomly selected pseudo-normal deviates (Φ_i). The E was generated as:

$$E = DD * \Phi_i$$

To generate deviates, D, a Cholesky decomposition was applied to the matrices. The decomposed matrix was post-multiplied by a vector of pseudo-random deviates N(0,1) which returned a vector of correlated pseudo-random numbers. In matrix notation,

$$\begin{bmatrix} D_1 \\ D_2 \\ D_3 \\ D_4 \\ D_5 \end{bmatrix} = \begin{bmatrix} \tau_{1,1} & \tau_{1,2} & \tau_{1,3} & \tau_{1,4} & \tau_{1,5} \\ 0 & \tau_{2,2} & \tau_{2,3} & \tau_{2,4} & \tau_{2,5} \\ 0 & 0 & \tau_{3,3} & \tau_{3,4} & \tau_{3,5} \\ 0 & 0 & 0 & \tau_{4,4} & \tau_{4,5} \\ 0 & 0 & 0 & 0 & \tau_{5,5} \end{bmatrix} * \begin{bmatrix} \Phi_1 \\ \Phi_2 \\ \Phi_3 \\ \Phi_4 \\ \Phi_5 \end{bmatrix}$$

where, D_i is the random multivariate normal deviate of the i^{th} trait, $\tau_{i,j}$ results from the Cholesky decomposition of genetic (co)variance matrix, Φ_i represents randomly selected pseudo-normal deviates for the i^{th} trait and 1, 2, 3, 4 and 5 represents milk yield, fat yield, protein yield, liveweight and longevity, respectively.

Table 7.3, 7.4, 7.5 and 7.6 show the genotypic and phenotypic parameters required by the simulation. All the genotypic and phenotypic parameters are contained in an input file and can thus be changed to simulate populations with different parameters and scenarios. The variance-covariance structure was assumed to be constant through the entire simulation period.

Table 7.2: Genotypic and phenotypic correlations between traits used in the model. Genotypic correlations are shown above the diagonal, heritabilities on the diagonal (bold) and phenotypic correlations below the diagonal

Traits	MY	FY	PY	Lwt	Longevity
MY	**0.26**	0.57	0.46	0.16	0.05
FY	0.63	**0.27**	0.82	0.66	0.13
PY	0.59	0.79	**0.25**	0.59	0.04
Lwt	0.13	0.67	0.65	**0.40**	0.07
Longevity	0.09	0.13	0.07	0.02	**0.05**

Legends: MY= Milk yield; FY = Fat yield; PY = Protein yield; Lwt = Liveweight

Table 7.3: Genotypic variance-covariance structure of different traits used in the simulation model. Genotypic covariances are shown above the diagonal and variances on the diagonal

Traits	MY	FY	PY	Lwt	Longevity
MY	17915.63	360.76	267.83	222.13	193.49
FY		22.36	16.87	32.37	20.51
PY			18.92	26.62	5.03
Lwt				107.58	20.99
Longevity					835.92

Legends: MY = Milk yield; FY = Fat yield; PY = Protein yield; Lwt = Liveweight

Table 7.4: Environmental correlations between traits used in the model

Traits	MY	FY	PY	Lwt	Longevity
MY	0.26	0.65	0.47	0.11	0.11
FY		0.27	0.77	0.68	0.40
PY			0.25	0.69	0.06
Lwt				0.4	0.01
Longevity					0.05

Legends: MY = Milk yield; FY = Fat yield; PY = Protein yield; Lwt = Liveweight

Table 7.5: Environmental variance-covariance structures of different traits used in the simulation model. Environmental covariances are shown above the diagonal and variances on the diagonal

Traits	MY	FY	PY	Lwt	Longevity
MY	34453.13	754.64	539.33	205.75	2552.92
FY		38.92	29.63	40.24	89.85
PY			37.09	39.64	51.05
Lwt				88.76	15.72
Longevity					15548.20

Legends: MY = Milk yield; FY = Fat yield; PY = Protein yield; Lwt = Liveweight

Table 7.6: Permanent environmental variance-covariance structure of different traits used in the simulation model. Permanent environmental covariances are shown above the diagonal and variances on the diagonal

Traits	MY	FY	PY	Lwt	Longevity
MY	16537.50	388.87	272.19	128.94	259.38
FY		21.53	16.05	27.07	9.80
PY			19.68	26.12	5.45
Lwt				72.62	2.08
Longevity					334.37

Legends: MY = Milk yield; FY = Fat yield; PY = Protein yield; Lwt = Liveweight

7.3.2 Population structure

The population of Pabna cattle consisted of about 10,000 cows distributed in 200 herds each with a herd size ranging from 40 to 60 cows with an age structures from 4 to 10 years to represent the likely herd composition of BMPCUL farmers. The base population at steady state simulated all the unrelated cows together. Ninety percent of the base cows were selected randomly for the next year. Offspring production and the phenotypic values of the base year cows were changed every year with the change of age and temporary environmental effects. For the production of offspring for the next generation, the biological and technical parameters from Table 7.7 were used. For all 20 years of simulation, the estimated breeding values (EBV) of longevity were set as functions, and 5% of cows were set for automatic culling every year as a fixed term according to the lower EBV of longevity. All base cows of the same years and progeny were kept together for further evaluation. The SAS codes for the simulation of the base herd and breeding populations are shown in Appendix 3(A).

Table 7.7: Population biological and technical parameters for the simulation study

Parameters	Parent-average testing	Progeny testing
a) Population parameters		
Number of cows	10,000	10,000
Bull to cow ratio		
For natural mating	1:20	1:20
For artificial mating	1:2000	1:2000
Percentage of bull dams	1.5	
Percentage of replacement	20	20
b) Survival and Reproduction		
Calving rate (%)	65	65
Survivability (%)	88	88
Calving interval (years)	1.3	1.3
Male and female calves ratio	1:1	1:1
c) Artificial insemination		
Number of straws/young bull	4,000	4,000
Number of straw required / pregnancy	2	3
Size of progeny group per testing bull		1:34

7.3.3 Genetic evaluation

Estimated breeding values (EBVs) were obtained from a univariate analysis of the base population and from a multivariate analysis of the later generations based on restricted maximum likelihood using the average information matrix as second derivatives in a quasi-Newton procedure (Johnson and Thompson, 1995). The model of analysis was presented as:

$$Y = Xb + Zu + e$$

where, Y is the traits yield,

e is the vector of error terms,

u is the vector of animal breeding value, random

Z is a matrix relating records with breeding values,

X is a matrix relating records with fixed effects,

b is a vector of fixed effects, considering all the effects used in the simulation model.

For the (co)variance of Y the assumption is:

var(u) = G

var(e) = R

and

cov(u,e) = 0

which gives

$$\text{var}(Y) = ZGZ' + R$$

A univariate animal model was used to estimate the breeding values of base population animals and then:

var(e) = R = Iσ^2

one random effect u = a,

design matrix Z = Z_a and

variance matrix G =A.σ_a^2,

where, A is the relationship matrix.

The mixed model equation (MME) thus became:

$$\begin{bmatrix} X'X & X'Z \\ X'X & Z'Z + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

After the base year, breeding values in later generations with all traits were estimated using multitrait repeatability animal model BLUP:

$$\begin{bmatrix}\mathbf{y}_1\\ \mathbf{y}_2\\ \mathbf{y}_3\\ \mathbf{y}_4\\ \mathbf{y}_5\end{bmatrix} = \begin{bmatrix}\mathbf{X}_1 & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{X}_2 & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{X}_3 & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{X}_4 & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{X}_5\end{bmatrix}\begin{bmatrix}\mathbf{b}_1\\ \mathbf{b}_2\\ \mathbf{b}_3\\ \mathbf{b}_4\\ \mathbf{b}_5\end{bmatrix} + \begin{bmatrix}\mathbf{Z}_1 & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{Z}_2 & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_3 & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{Z}_4 & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{Z}_5\end{bmatrix}\begin{bmatrix}\mathbf{u}_1\\ \mathbf{u}_2\\ \mathbf{u}_3\\ \mathbf{u}_4\\ \mathbf{u}_5\end{bmatrix} + \begin{bmatrix}\mathbf{W}_1 & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{W}_2 & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{W}_3 & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{W}_4 & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{W}_5\end{bmatrix}\begin{bmatrix}\mathbf{p}_1\\ \mathbf{p}_2\\ \mathbf{p}_3\\ \mathbf{p}_4\\ \mathbf{p}_5\end{bmatrix} + \begin{bmatrix}\mathbf{e}_1\\ \mathbf{e}_2\\ \mathbf{e}_3\\ \mathbf{e}_4\\ \mathbf{e}_5\end{bmatrix}$$

Var(u)= $A\sigma_u^2$,

Var(p)= $G\sigma_p^2$

Var (e)= I σ_e^2 and

Cov(u,p) =Cov(u,e)= Cov(p,e) =0

which gives

$$\text{var}(Y) = ZAZ' + WGW' + R$$

The mixed model equation (MME) for the multivariate animal model became:

$$\begin{bmatrix} X'X & X'Z & X'W \\ X'X & Z'Z + A^{-1}\alpha_1 & Z'W \\ W'X & W'Z & W'W + G^{-1}\alpha_2 \end{bmatrix}\begin{bmatrix}\hat{b}\\ \hat{u}\\ \hat{p}\end{bmatrix} = \begin{bmatrix}X'y\\ Z'y\\ W'y\end{bmatrix}$$

Where, $\alpha_1 = \frac{\sigma_e^2}{\sigma_u^2}$ and $\alpha_2 = \frac{\sigma_e^2}{\sigma_p^2}$

7.3.4 Selection by using pedigree information

Selection based on total merit, was carried out on bulls, heifers and cows. All four (cows to breed cows, cows to breed bulls, bulls to breed cows and bulls to breed bulls) selection pathways were considered for the estimation of genetic gains. The mortality and culling rate for conformation and semen quality of bulls was considered as 12% from 5, 6, and 7 years old. In each year, 5 bulls were selected from the bull calves born in the herd for the production of breeding bulls and female replacements on the basis of their dam's merit. The number of cows to be inseminated was calculated according to the mating strategy of this model. It was assumed that on average 12,000 semen doses per year were used per bull, and that each bull was available for up to 3 years in the breeding programme.

Each year, 150 selected active cows were mated to the 5 selected bulls. In year one, the best base bulls were mated with all base cows for the production of progeny. It was assumed that the average breeding value for year one was zero. From the year one population, the best cows and bulls were selected and mated together and their average breeding values increased with the subsequent years of selection and mating. From year one to four the same best base bulls were used for the production of progeny. However, from years 5 to 20, the best bulls and cows from progeny born in year one were selected and mated for the production of progeny. Each year, 20% of the base cows were replaced by heifers. In the breeding scheme, cows were used up to 10 years of age, therefore by the 9th year of simulation, the entire base herd was replaced by cows of higher genetic merit. The average genetic merit of all cows born in a particular year was considered as the average genetic merit of the herd for the purpose of calculating the rate of genetic gain. Because of the time taken to replace base cows, the calculation of genetic gain was calculated in 3 periods. Firstly, from the base year to year 9, secondly, from year 9 to 20 years and thirdly an overall gain from the base year to year 20. The asymptotic genetic gain for this population was derived by calculating the year-by-year change in genetic values.

7.3.5 Selection by using progeny testing

In the cooperative dairying conditions of Bangladesh, the farmer members are more organised, and currently keep individual cow performance records. For progeny testing purposes, some herds of the selected farmers from the primary societies of

BMPCUL were used. A total of 1400 cows from different herds were selected for the progeny testing purpose. The number of bulls required annually for the progeny testing herd is approximately 40 according to Robertson (1957). The formula for the optimum group size is:

$$n = 0.56\sqrt{\frac{K}{h^2}}$$

where, h^2 is the heritability of the traits and K = ratio of required number of sires for breeding, and the total number of sires selected.

In this progeny testing scheme, herd bulls are used by natural service. Thus the number of bulls needed in this scheme is rather high, and consequently they had to be partly bred within the herd itself. The young bulls used for test insemination were selected from the 150 active cows. After progeny testing the bulls, only the best five bulls were selected for the production of replacement bulls and cows, on the basis of their progeny merit.

The selection objective was based on the improvement of milk yield, fat yield, protein yields, liveweight and longevity. Progeny tests were completed when the bulls were 8 years old because the bulls entered into the progeny testing programme when they were 4 years old.

The mating strategy was similar to that described in 7.3.4. Each year the model calculated the genetic merit of new progeny, as the average of the genetic superiority of the selected parents.

7.3.6 Scenarios between selection objectives and selection schemes

Genetic gain and correlated responses were evaluated within six scenarios that combined three selection objectives and two selection schemes as follows:

Selection objectives:

i. Selection for milk production
ii. Selection for milk and survivability
iii. Selection for total merit

Selection schemes:

i. Selection on progeny performance
ii. Selection on parent average

In this simulation study the selection intensities for parent average ($\bar{i} = 1.55$) and progeny performance ($\bar{i} = 1.64$) schemes were based on the four pathways of selection and differed because of the different breeding structure of the two schemes.

The economic selection index value of the selection objective of milk production was calculated by the product of breeding values, and the economic values of all traits. For this objective, the economic value of milk yield only was used, with the economic value of all other traits being set to 0. The economic selection index value for the selection objective of milk and survivability was calculated by the product of breeding values and the economic values of the two traits; the economic value of the remaining traits was set to 0. For the selection objective of total merit, the economic selection index value was estimated as the product of breeding values and the economic values of all traits.

An estimate of T (known as total merit) was calculated as:

Total merit (T) = $V_{MY}EBV_{MY}+V_{FY}EBV_{FY}+V_{PY}EBV_{PY}+V_{Lwt}EBV_{Lwt}+V_{Longe}EBV_{Longe}$

where EBV_{MY}, EBV_{FY}, EBV_{PY}, EBV_{Lwt} and EBV_{Longe} are the estimated breeding values for each trait and

V_{MY}, V_{FY}, V_{PY}, V_{Lwt} and V_{Longe} are the respective economic values

Selection responses for milk yield, fat yield, protein yield, liveweight and longevity were calculated from the regression of traits values on the selection index, which were obtained from the best linear unbiased prediction (Henderson, 1963).

The model started with the creation of the base animals and considered herd size and age structure with two selection schemes and three selection objectives. All combinations were simulated with at least ten replicates. Within each replicate, breeding values and the realised observations for all animals were stored. From this data the average genetic merit for animals born within a year were calculated. Yearly results from all simulation models were analysed in a model, taking account of the two main factors being investigated. Analyses were carried out using Proc Mixed in SAS (Littell et al., 1996).

7.3.7 Correlated response to selection

Stochastic simulation allowed the estimation of correlated responses of all traits considered in the simulation. Graphs of correlated traits were constructed allowing for 20 years set on the x axis with the economic merit of different traits in the breeding objectives being set on the y axis.

7.3.8 Genetic gain calculated deterministically

Genetic gain per year was calculated for milk, fat, protein yield, liveweight and longevity using a deterministic approach to compare with the results obtained from the stochastic approach. The method was described in section 6.3.7 (Chapter 6).

7.4 Results

The annual rates of genetic gain in the objective traits following 20 years of selection for the two different breeding schemes and three selection objectives for cows are shown in Tables 7.8, 7.9 and 7.10. The rate of genetic gains of these traits on time for 20 years selection and mating for breeding bulls (selected bull from a particular year born bull) in respect of the above scenarios are presented in Table 7.11.

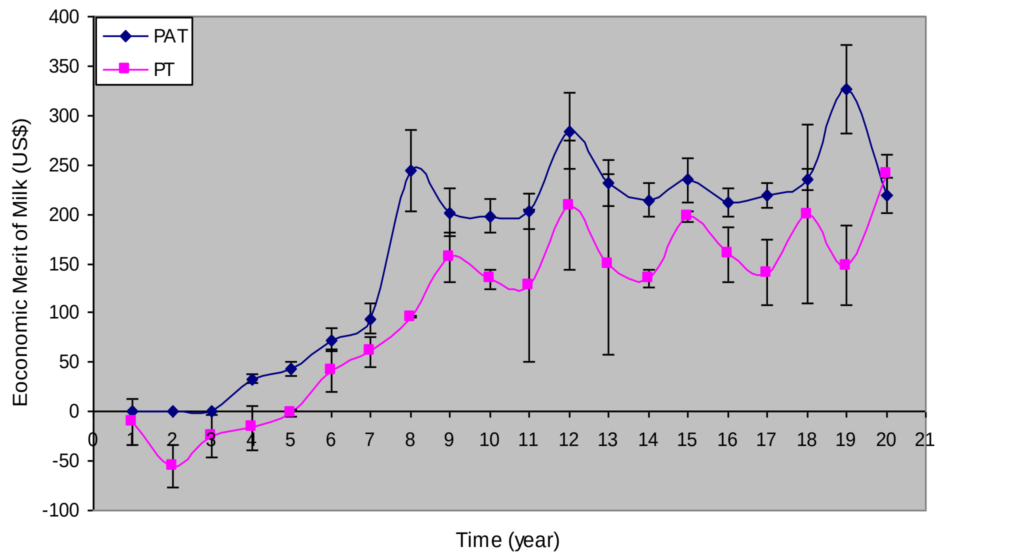
The changes of a particular year born cow's (all) average economic merit (US$) with standard deviation (bar) for milk yield of milk merit (US$), milk and survivability merit (US$) and total merit (US$) over 20 years are shown in Figures 7.1, 7.2 and 7.3 and for selected bulls in Figures 7.4, 7.5 and 7.6 for the two breeding schemes and the three selection objectives. The equivalent plots of average economic merit (US$) with standard deviation (bar) for fat yield, protein yield, liveweight and longevity for all cows are in Appendix 3.B (Figures 7.7 to 7.9) and for selected bulls are in Appendix 3.B (Figures 7.10 to 7.12) are presented.

7.4.1 Shape of the curves for responses of different traits

From the Figures 7.1 to 7.6 a rapid response was observed from the base year up to year 9, after which the rate of increase became slower for all traits up to year 20 of the simulation. The shape of the responses was varied according to the differences of sex, breeding schemes and selection objectives.

Figures 7.1 to 7.3 showed that under both breeding schemes from year 1 to year 4, the rate of genetic gains was very low and even negative. Figure 7.1 showed that rapid genetic progress was achieved in both selection schemes from year 6 to 8; after which it diminished to year 11, and from year 11 to 12 once again high responses were observed and subsequently, to year 20, the asymptotic response had appeared. Figure 7.2 shows that genetic progress steadily increased from year 5 to 12 in the parenet-average testing selection scheme and figure 7.3 shows the rapid increase of genetic gains from year 4 to 7, following which it declined, in case of the parent average testing breeding scheme. However, for all the selection objectives, the genetic gains of the milk yield were shown to be steady under progeny testing breeding schemes. For bulls, figures, 7.4, 7.5 and 7.6 also show the steady progress of all the selection objectives, in both breeding schemes. Similar trends were achieved for fat yield, protein yield, liveweight and longevity for both cows and breeding bulls (Appendix 3.B, Figures 7.10 to 7.11.

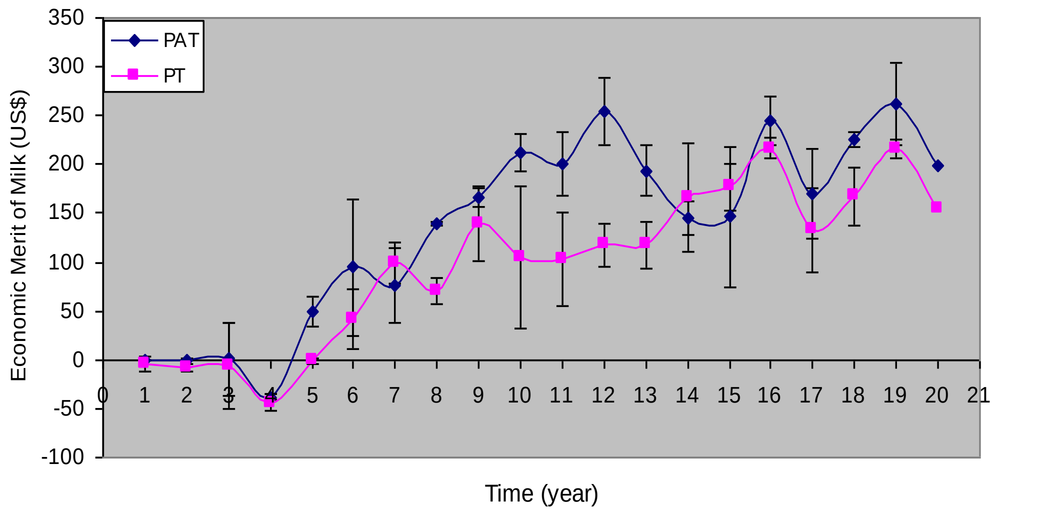
Figure 7.1. Average economic merit (US$) with standard deviation (bar) for milk yield under parent average testing (PAT) and progeny testing (PT) breeding schemes with a selection objective of milk merit for all cows born in a particular year



7.4.2 Responses of different traits in cows vs. bulls

Tables 7.8 to 7.11 show that the annual rate of genetic gains from year 1 to 20 of different traits, varied between cows and selected bulls under the two different breeding schemes in three different selection objectives. In the selection objective of milk merit under parenet average testing breeding scheme, the genetic gains for milk yield, fat yield and protein yield were similar in cows and bulls but the responses of liveweight and longevity for bulls were higher than the cows. Similar results were obtained under the progeny testing breeding scheme, except for the protein yield, which was higher in cows than in bulls. In the selection objective of milk and survival merit under the parent average testing breeding scheme, the genetic gains for milk yield and liveweight was higher in bulls than cows, but that all other traits indicated similarly. In this selection objective, under the progeny testing breeding scheme, the longevity of cows was higher than bulls, and all other objective traits showed similar responses for both cows and bulls. The annual rate of genetic gains in the selection objective, total merit under parent-average testing breeding scheme were shown to be similar to the selection objective, milk and survival merit. The only differences were observed in longevity and protein yield under the progeny testing breeding scheme between bulls and cows.

Figure 7.2. Average economic merit (US$) with std. deviation (bar) for milk yield under parent average testing (PAT)and progeny testing (PT) breeding schemes with a selection objective of milk and survivability merit for all cows born in a particular year



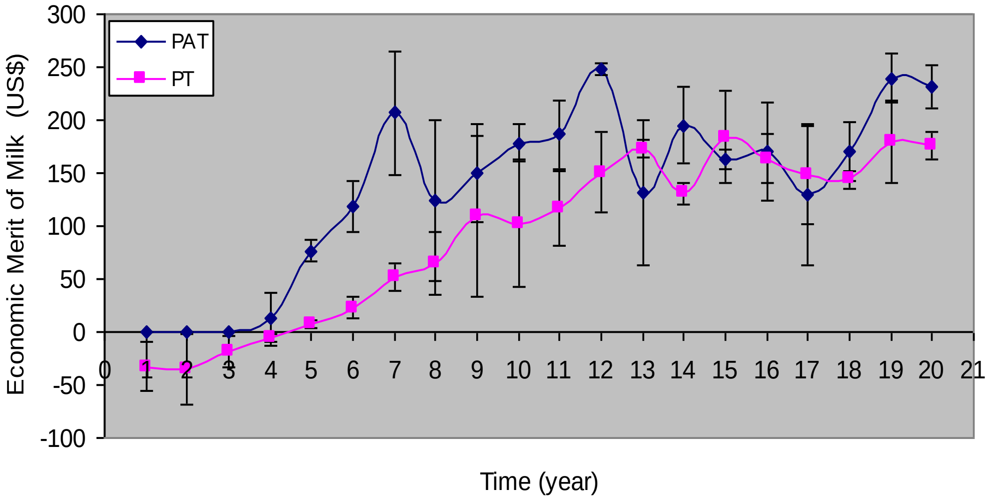
7.4.3 Responses of traits under different selection objectives and the breeding schemes

Within the selection objectives between the breeding schemes, the annual rate of genetic gains for milk yield, liveweight and longevity were significantly different. The responses for milk yield of the parent-average testing breeding scheme, under the milk merit objective, was significantly higher than the total merit selection objective for cows from the base year up to year 20. The annual rate of genetic gains for fat yield and protein yield did not reveal any differences between selection objectives within the breeding scheme.

From the base year up to year 9, the parent-average testing breeding scheme showed comparatively higher responses for all traits, in the three different selection objectives, compared with the progeny testing breeding scheme. The trends of genetic gains of different traits within selection objectives showed differences between parent-average and progeny testing breeding schemes.

The annual rates of genetic gain of different traits were varied, dependent on the selection objectives for both cow and bull population. From Tables 7.8 to 7.10 it was shown that from year 1 to 9, and from year 9 to 20, the responses of all the traits in the selection objective, milk merit, was higher than the other two selection objectives for cows. In the responses of all the traits in the selection objectives, total merit was lower than the other two objectives, and the milk and the selection objective, and that milk and survival merit was intermediate for cows. Similar findings were observed in the case of breeding bulls.

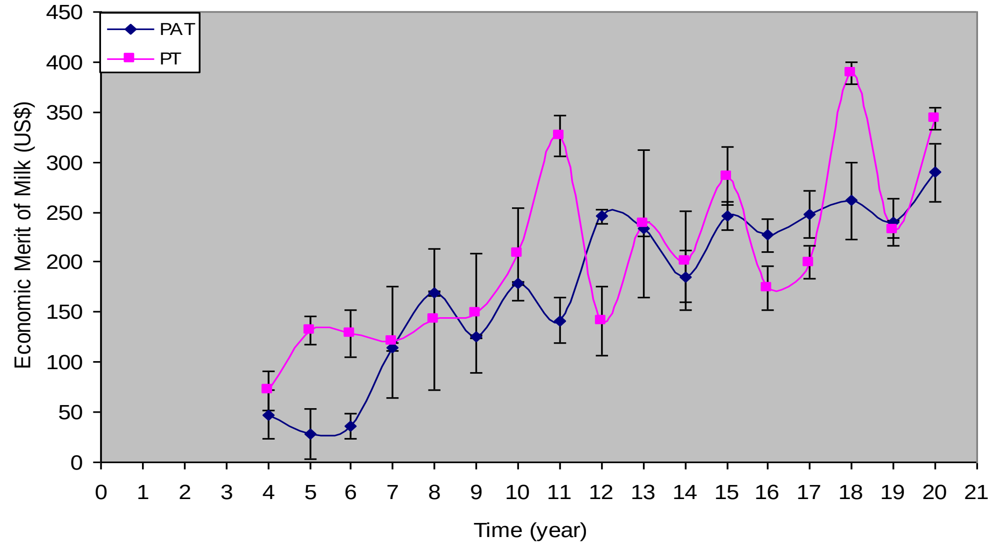
Figure 7.3. Average economic merit (US$) with standard deviation (bar) for milk yield under parent average testing (PAT) and progeny testing (PT) breeding schemes with a selection objective of total merit for all cows born in a particular year



7.4.4 Responses of individual traits

The responses in individual traits also differed between breeding schemes within the selection objective, and also between selection objectives and sexes over a 20 year simulation period. The highest genetic gain (US$ 15.03/year or 29.3 litre milk/year) was achieved when the selection objective was for milk yield genetic merit compared with US$ 10.95/year or 21.2 litre/year when selection was on total genetic merit over 20 years of selection, and mating under the parent-average testing breeding scheme. However, a lower genetic gain for longevity was observed in those scenarios. The genetic gains for milk yield in consideration of both selection scheme and three selection objectives ranged from US$ 12.0/year or 23.3 litre/year to US$ 13.5/year or 26.2 litre milk/year for 20 years of selection and mating under progeny testing. The genetic gains of protein yield and liveweight, in the selection objective total merit under parent-average testing breeding scheme was lower than all other selection objectives, and also the progeny testing breeding scheme in this selection objective. However, for all other traits in the three selection objectives, under the parent-average and progeny testing breeding schemes, showed only intermediate responses.

Figure 7.4. Average economic merit (US$) with standard deviation (bar) for milk yield under parent average testing (PAT) and progeny testing (PT) breeding schemes with a selection objective of milk merit for selected bulls in a particular year



In the case of breeding bulls the genetic gains for all traits within three selection objectives, the milk merit and milk and survival merit were shown to be better than the total merit objective. However, the rate of genetic gains for fat yield, protein yield and liveweight in milk merit and milk and survival merit, under a parenet-average testing breeding scheme, showed highly significant differences than total merit. On the other hand, under the progeny testing breeding scheme, there were no differences found in milk yield, fat yield and liveweight in between selection objectives.

Figure 7.5. Average economic merit (US$) with std. deviation (bar) for milk yield under parent average testing (PAT) and progeny testing (PT) breeding schemes with a selection objective of milk & survivability merit for selected bulls in a particular year

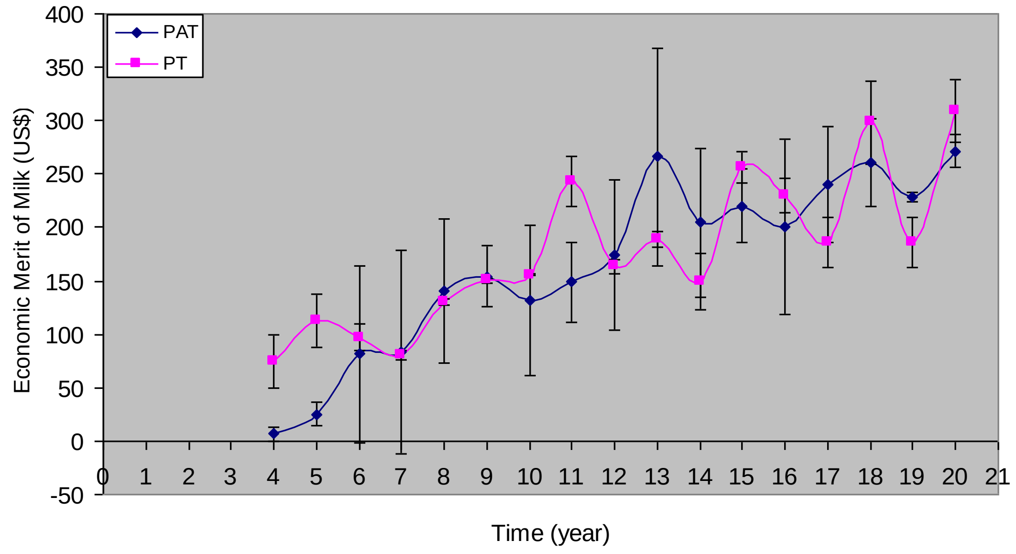
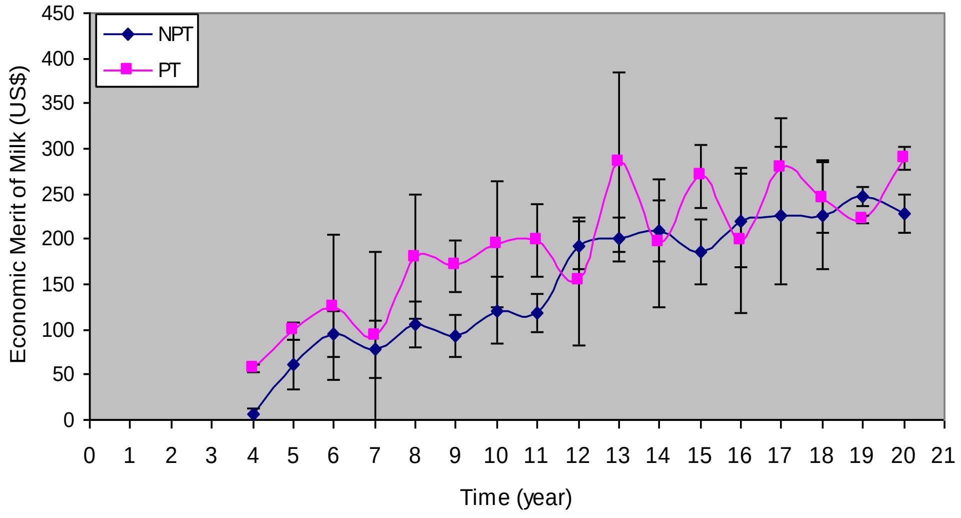


Figure 7.6. Average economic merit (US$) with standard deviation (bar) for milk yield under parent average testing (PAT) and progeny testing (PT) breeding schemes with a selection objective of total merit for selected bulls in a particular year



7.4.5 Stochastic vs. deterministic responses

For the comparisons of results obtained from the stochastic simulation model, the annual rate of genetic gain per year for different traits were estimated deterministically using the four pathways (Rendel and Robertson, 1950) using the additive genetic and total phenotypic (co)variance relationships and economic weights of different traits (Table 7.12). Genetic gain of individual traits per generation were obtained deterministically in Chapter 6 using similar (co)variances and economic values of the trait but with no consideration of selection pathways.

7.4.6 Correlated responses

The correlated responses with longevity, and all other traits in the selection objectives for the two breeding schemes, are shown in Table 7.13. Positive responses were observed for all the traits, and lower responses were observed in the selection objective, milk merit under both breeding schemes than in the other two selection objectives.

Table 7.8: Mean and standard error (se) of genetic gain (Δg) in US$ per year and R^2 value of milk traits, liveweight and longevity of the simulated cow population under parent average and progeny testing selection schemes with a selection objective for milk merit

Traits	Selection for milk merit																	
	PAT									PT								
	From year 1 to 9			From year 9 to 20			From Year 1 to 20			From year 1 to 9			From year 9 to 20			From year 1 to 20		
	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2
MY	29.4[b]	0.70	0.81	4.20[ab]	0.25	0.16	15.03[b]	0.13	0.74	22.50[a]	0.97	0.80	4.56	0.31	0.21	13.5[a]	0.45	0.80
FY	0.69	0.03	0.89	0.07	0.02	0.12	0.29	0.03	0.70	0.60	0.10	0.70	0.11	0.05	0.22	0.24	0.02	0.66
PY	0.61	0.03	0.89	0.11	0.02	0.29	0.27	0.03	0.76	0.50	0.07	0.80	0.07	0.07	0.11	0.23	0.01	0.69
Lwt	0.50	0.10	0.78	0.05	0.03	0.08	0.19[a]	0.03	0.66	0.50	0.12	0.90	0.10	0.04	0.10	0.27[b]	0.05	0.75
Longe	1.30	0.20	0.65	1.20[b]	0.08	0.56	1.06[a]	0.12	0.74	1.20	0.24	0.80	0.97[a]	0.28	0.29	1.50[b]	0.38	0.79

Legends: PAT = Parent average testing breeding scheme; PT = Progeny testing breeding scheme; MY = Milk yield; FY = Fat yield; PY = Protein yield; Lwt = Liveweight; Longe = Longevity.

Means with superscript a and b are different at 5% level of significance between breeding schemes within selection objectives.

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Table 7.9: Mean and standard error (se) of genetic gain (Δg) in US$ per year and R^2 value of milk traits, liveweight and longevity of the simulated cow population under parent average and progeny testing selection schemes with a selection objective for milk and survivability merit

Traits	Selection for milk and survivability merit																	
	PAT									PT								
	From year 1 to 9			From year 9 to 20			From Year 1 to 20			From year 1 to 9			From year 9 to 20			From year 1 to 20		
	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2
MY	22.7[b]	1.6	0.79	2.6[a]	0.04	0.10	13.7[b]	0.64	0.77	18.5[a]	0.47	0.71	6.99[b]	0.23	0.42	12.1	0.35	0.82
FY	0.65	0.11	0.90	0.01[a]	0.01	0.10	0.30	0.01	0.64	0.55[b]	0.01	0.82	0.28[b]	0.02	0.53	0.28	0.03	0.82
PY	0.39	0.02	0.87	0.02[a]	0.01	0.01	0.23	0.02	0.65	0.30	0.10	0.76	0.25[b]	0.10	0.69	0.24	0.04	0.85
Lwt	0.25[a]	0.02	0.58	0.04[a]	0.01	0.07	0.14[a]	0.01	0.51	0.40[b]	0.10	0.78	0.36[b]	0.05	0.59	0.33[b]	0.03	0.83
Longe	0.88[a]	0.12	0.64	2.05[b]	0.32	0.33	1.65[a]	0.45	0.45	1.9[b]	0.27	0.83	1.56[a]	0.24	0.87	2.70[b]	0.16	0.83

Legends: PAT = Parent average testing breeding scheme; PT = Progeny testing breeding scheme; MY = Milk yield; FY = Fat yield; PY = Protein yield; Lwt = Liveweight; Longe = Longevity.

Means with superscript a and b are different at 5% level of significance between breeding schemes within selection objectives.

Table 7.10: Mean and standard error (se) of genetic gain (Δg) in US$ per year and R^2 value of milk traits, liveweight and longevity of the simulated cow population under parent average testing and progeny testing selection schemes with a selection objective for total merit

Traits	Selection for total merit																	
	PAT									PT								
	From year 1 to 9			From year 9 to 20			From Year 1 to 20			From year 1 to 9			From year 9 to 20			From year 1 to 20		
	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2
MY	25.2[b]	0.37	0.74	3.70[a]	1.01	0.1	10.95[a]	0.04	0.62	17.7[a]	1.71	0.94	5.07[b]	0.32	0.53	12.0[b]	0.16	0.89
FY	0.61[b]	0.01	0.93	0.10	0.03	0.1	0.25	0.01	0.67	0.40[a]	0.12	0.93	0.13	0.03	0.34	0.27	0.04	0.85
PY	0.50	0.03	0.91	0.10	0.01	0.05	0.17[a]	0.01	0.55	0.44	0.12	0.87	0.11	0.04	0.35	0.25[b]	0.10	0.83
Lwt	0.45	0.03	0.89	0.03[a]	0.02	0.02	0.17[a]	0.02	0.55	0.40	0.08	0.90	0.10[b]	0.0	0.44	0.27[b]	0.01	0.85
Longe	3.08[b]	0.12	0.61	1.95[a]	0.02	0.29	2.80	0.21	0.75	2.6[a]	1.73	0.72	2.60[b]	0.63	0.55	2.77	0.78	0.84

Legends: PAT = Parent average testing breeding scheme; PT = Progeny testing breeding scheme; MY = Milk yield;
FY = Fat yield; PY = Protein yield; Lwt = Liveweight; Longe = Longevity.

Means with superscript a and b are different at 5% level of significance between breeding scheme within selection objectives.

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Table 7.11: Mean and standard error (se) of genetic gain (Δg) in US$ per year and R^2 value of milk traits, liveweight and longevity of the simulated breeding bulls under different breeding schemes in three selection objectives

Traits	Selection for milk merit						Selection for milk and survivability merit						Selection for total merit					
	PAT			PT			PAT			PT			PAT			PT		
	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2	Δg	se	R^2
MY	15.08^{b}	0.33	0.90	12.89	0.63	0.55	14.85^{ab}	0.56	0.86	11.69	0.32	0.68	13.49^{a}	0.41	0.91	11.86	0.53	0.73
FY	0.27^{b}	0.10	0.94	0.26	0.02	0.54	0.27^{b}	0.02	0.81	0.20	0.01	0.48	0.18^{a}	0.02	0.68	0.23	0.05	0.46
PY	0.25^{b}	0.04	0.84	0.17^{a}	0.05	0.45	0.24^{b}	0.02	0.71	0.26^{b}	0.03	0.64	0.17^{a}	0.03	0.61	0.19^{a}	0.1	0.45
Lwt	0.27^{b}	0.01	0.74	0.38	0.1	0.48	0.23^{b}	0.04	0.56	0.31	0.06	0.44	0.17^{a}	0.02	0.50	0.30	0.04	0.27
Longe	2.18^{b}	0.23	0.80	2.86^{b}	0.14	0.63	1.46^{a}	0.37	0.53	1.51^{a}	0.19	0.49	1.69^{a}	0.13	0.69	2.06^{b}	0.86	0.48

Legends: PAT = Parent-average testing breeding scheme; PT = Progeny testing breeding scheme; MY = Milk yield;
FY = Fat yield; PY = Protein yield; Lwt = Liveweight; Longe = Longevity.

Means with superscript a and b are different at 5% level of significance between selection objectives within breeding scheme.

Table 7.12: Annual rate of genetic gain (Δg) for different traits by a deterministic approach in consideration of the four pathways of selection

Traits	Selection strategy					
	Selection for milk merit		Selection for milk and survivability merit		Selection for total merit	
	PAT	PT	PAT	PT	PAT	PT
MY	15.90	15.42	15.27	14.81	16.59	14.61
FY	0.32	0.16	0.35	0.18	0.15	0.13
PY	0.24	0.12	0.24	0.12	0.10	0.09
Lwt	0.38	0.19	0.45	0.22	0.10	0.08
Longe	0.03	0.02	0.51	0.25	0.27	0.23

Legends: MY = Milk yield; FY = Fat yield; PY = Protein yield; Lwt = Liveweight; Longe = Longevity
PAT = Parenta average testing breeding scheme and PT = progeny testing breeding scheme.

Table 7.13: Correlated response (CR_Y) with longevity and other traits in consideration of two breeding schemes within three selection objectives

Traits	Selection strategy					
	Selection for milk merit		Selection for milk and survivability merit		Selection for total merit	
	PAT	PT	PAT	PT	PAT	PT
MY	2.31	2.51	4.93	4.77	5.72	4.88
FY	0.07	0.09	0.16	0.19	0.16	0.18
PY	0.04	0.07	0.12	0.21	0.11	0.14
Lwt	0.04	0.08	0.12	0.22	0.07	0.26

Legends: MY = Milk yield; FY = Fat yield; PY = Protein yield; Lwt = Liveweight; Longe = Longevity
PAT = Parenta-average testing breeding scheme and PT = progeny testing breeding scheme.

7.5 Discussion

In this study a multitrait stochastic simulation model was developed to represent selection and straightbreeding systems for Pabna cattle. In this model the additive genetic effects, permanent and temporary environmental effects, herd and age effects were included along with Mendelian sampling and inbreeding effects.

7.5.1 Shape of the curves for responses of different traits

The genetic gains for all the traits in both selection schemes and three selection objectives showed rapid progress from the base year up to year 9. The primary reason for this rapid gain in early years than later years, is that it requires 9 years for all the unimproved base cows in the herd to be replaced.

Figures 7.1 and 7.2 showed that genetic trends up to year 4 were zero or negative, and that the genetic gain started from year 5 onwards. Cows calved at 4 years of age therefore, up to year 4 the base cows and base bull were used for the production of progeny. For this reason lower genetic trends might have occurred up to year 4.The selected bulls and cows have their first progeny in year 5. However, from year 5 and through the remaining years, the male and female progeny born by birth year 1 and onward were used. From Figure 7.1 and Appendix 3.B (Figure 7.7) it is seen that rapid responses for milk, fat, protein yield and liveweight were achieved in years 6 to 8, and then slightly less and steady up until year 11, and again rapidly in years 11 to 12, then another decline, and steady progress occurred. The higher genetic gains obtained in those particular years might be due to the effects of sires and dams. Genetic potentiality of parents was then passed on to the progeny, leading to higher genetic gains in upcoming generation. Similar results were reported by Dzama et al. (2001). For breeding bulls, a comparatively lower rate of genetic gain was achieved compared with cows under parent average and progeny testing breeding schemes for all the selection objectives of all the traits (Figure 7.4 to 7.6 and Appendix 3.B, Figures 7.10 to 7.12). In this study only 40 bulls were produced from 150 active cows and out of 40 bulls only 5 selected bulls were used in breeding purpose. Therefore, the lower genetic trends may be due to the small number of bulls were simulated in this study which allowed to provide lower selection intensities, which leading to this phenomenon.

7.5.1 Responses of different traits in cows vs. bulls

The annual rates of genetic gain differed between cows and bulls. This might be due to the differences of sexes and, also the effects of selection intensities. The selection intensities have a positive impact on responses (Rendel and Robertson, 1950). The annual rate of genetic gain for fat yield and protein yield, had no significant differences, between cows and bulls but in the case of liveweight and longevity, the breeding bulls (selected bull population) were higher than cows in both parent average and progeny testing breeding schemes in all three selection objectives. This high value was reflected in the high intensity of selection among bulls. Similar findings were reported for response of liveweight by Dzama et al. (2001).

7.5.3 Responses of traits under different selection objectives and breeding schemes

The responses for all traits in all three selection objectives were higher in the parent average than the progeny testing breeding scheme except liveweight. This might have been caused by there being only a small number of bull used and also small herd size being simulated. In the parent average testing breeding scheme, only 5 superior bulls were selected each year. But in the progeny testing breeding scheme, 40 bulls were progeny tested with 1400 cows each year and all cows were considered in this simulation. This may have lead to lower responses per year, as all bulls were involved in progeny testing, and more than 50% of the bulls were below average. In addition, 150 active cows were selected for the production of breeding bulls. This could have affected the lower genetic gains per year. In this simulation study, the selection intensities, accuracy of selection and generation interval was 1.55 vs. 1.64, 0.57 vs. 0.59 and 6.3 year vs. 8 years, respectively for parent average vs progeny testing breeding schemes were used in consideration of all selection pathways. The higher generation intervals and accuracies could also be a cause of lower genetic gains under progeny testing. The numbers of active cows selected from the total population have led to selection intensities and thus, genetic gains. Similar results were reported by Shannon et al. (1984), Dekkers (1992), Everett (1984), Randel and Robertson (1950) and Skjervold (1963), who concluded that the size of the active cow population (potential bull mothers) has a significant effect on the rate of genetic gain, because high selection intensities can be achieved in the selection of bull mothers.

The genetic gains for milk yield per cow per year, of the parent-average testing breeding scheme, exhibited 10% and 11% higher in the milk merit and milk and survivability merit objectives, respectively, than the progeny testing breeding scheme.

The differences in genetic gains between selection objectives were found and these differences were occurred due to the differences of the economic values of the construction of the economic merit under the different selection objectives. The bulls were selected on the basis of their mothers' genetic merit. In this simulation, only the milk and survivability had positive economic values and other traits were negative, and the economic values arose from the milk payment system. Sørensen et al. (2006) observed the lower genetic gains for selection of the milk merit compared with selection of cows for total merit. In their simulation they used positive economic values for all traits.

7.5.4 Genetic gain in individual traits

The genetic gains in individual traits varied. This variation was due to the differences in breeding schemes and selection objectives. The differences in selection strategies on genetic gains were reported by Sørensen et al. (2006). Furthermore, the differences might be due to the differences of the economic values of the traits. The total genetic merit resulted more from the cost reducing traits (longevity) than the production traits (milk, fat and protein yield). Similar findings were reported by Lassen et al. (2007) and Besbes et al. (2002). Besbes et al. (2002) obtained higher total merit index from the cost reducing traits and less increase in production traits, from the collected data of individual cow's.

In the current model, from year 1 to 20 under all three selection objectives, the annual genetic progress obtained was from 1.2 to 1.6% and from 1.3 to 1.5%, of the mean in the parent average testing, and the progeny testing selection schemes, respectively. These values were higher than that of Lee et al. (1985) but lower to Specht and McGilliard (1960). Lee et al. (1985) estimated that the annual genetic progress in the registered Holstein female population was less than 1% of the mean and Specht and McGilliard (1960) estimated that more than 2% per year for artificially inseminated populations.

7.5.5 Stochastic vs. deterministic responses

Similar base genotypic and phenotypic (co) variances and economic values were used for the derivation of genetic gains for the different traits under both stochastic and deterministic approach, and similar results (e.g. Table 7.8 and Table 7.12) were obtained. These indicate that the responses obtained from the stochastic simulation model were validated. Furthermore, the genetic gain for milk yield, fat yield and protein yield was predicted at US$49.65i, US$0.76i and US$4.15i per generation for Pabna cattle through the deterministic approach irrespective of selection pathways and are presented in Chapter 6. If the similar selection intensity ($\bar{i} = 1.55$) and generation interval (6.33) for parent average breeding scheme of stochastic approach is considered then the annual rate of genetic gain for milk yield, fat yield and protein yield become US$12.2, US$0.20 and US$1.02, respectively (Chapter 6). In considering stochastic approach under three selection objective, the achieved genetic gain ranged from US$11 to US$16 for milk yield, from US$0.22 to US$0.30 for fat yield and from US$ 0.19 to US$0.29 for protein yield on a per cow per year basis, from the base year to 20 years of the simulation from parent average and progeny testing breeding schemes. These figures suggest that the multitrait stochastic deterministic models gave similar results which suggest the stochastic model gives realistic results.

7.5.6 Correlated responses

Positive correlated responses were observed for all the traits (Table 7.13), which indicated that selection for longevity could be achieved through selection for one or more associated traits. However, different responses between selection schemes within a selection objective and between selection objectives were found. In this simulation, longevity was set to a function, that is, 5% of low survival cows were culled automatically during each year’s simulation and leaving the higher longevity animals in the herd. This leads to higher genetic gains for all the traits as a positive correlated response. This could have increased the longevity of the cows. Similar findings were observed by Madgwick and Goddard (1989) and Wall et al. (2003).

Madgwick and Goddard (1989) stated that increasing longevity reduces replacement costs, changing herd structures to a higher proportion of older cows in the herd, allowing for an increased culling level for milk production which leads to increased farm profits. Essl (1998) reported that selection on determinants of both involuntary culling, and on measurements of longevity, may be used as selection objectives to improve longevity.

7.6 Conclusion

Using a stochastic model, all breeding animals were simulated under either a progeny or a parent average testing breeding scheme with three selection objectives. The simulation study showed that the rate of genetic gains differ, according to selection schemes and objectives. Selection of animals under parent average testing breeding schemes produced better in milk merit and milk and survivability merit objective than the progeny testing breeding scheme. The model offered an opportunity to utilise longevity as a functional trait, leading to a higher productivity of cows, by increasing the productive life or herd life of the cows. The model developed in this study offers breeders from Bangladesh an opportunity to compare different selection objectives, and also evaluate different breeding schemes.

7.7. References

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CHAPTER EIGHT

General Discussion

8.1 General discussion

The total human population of Bangladesh is about 141 million (BBS, 2007), and the total dairy cattle population is 10.5 million (DLS, 2002). If every person in Bangladesh consumed 120g of milk per day (as fluid or processed in any form), the current annual milk demand would be about 6 million tonnes. This is over two and half times the recorded milk production of Bangladesh (FAO, 2004). To offset this shortfall, Bangladesh imports milk from developed countries at the expense of hard earned foreign currency. Meeting Bangladesh’s demand for milk is an important national objective. The goal of the government is to increase the output and efficiency of its milk supply, and ensuring adequate nutrition at acceptable prices. The daily milk yield of a local Bangladeshi cow is very low, being about 1.5 liters of milk (Hossain et al., 2002 and Hirooka and Bhuiyan, 1995). Therefore, priority must be given to increasing the milk (and meat) productivity of animals through better management, feeding, animal health and genetics. The low productivity of cows contributes to low farm profit, so increasing milk (and meat) production has the added benefit of improving the financial variability of farms.

The present study is focused on the development of models for dairy cattle’s genetic improvement under cooperative dairying in Bangladesh. The main aims of this thesis were to examine genetic approaches to assist with improving milk yield from dairy cattle, to meet the nutritional demands of Bangladeshi people and to make some recommendations as to the future direction of genetic research. The issues considered in this thesis were the prediction of 270-day milk yields based on various mathematical models to represent lactation curves (chapter 4), the development of a deterministic farm model to represent the costs, revenue and profits of individual cows, and also the whole farm (Chapter 5), the derivation of economic values using profit functions for traits included in breeding objectives and genetic gains in these traits (Chapter 6) and a multitrait stochastic simulation model for predicting the genetic merit of individual cows under progeny and parent-average testing breeding schemes with three different selection objectives (Chapter 7).

8.2 Meeting milk demand in Bangladesh

The Bangladesh dairy population consists of many breeds and their crosses. There are no accurate population statistics by breed of dairy cattle in Bangladesh. However, about 80% of the cows are the indigenous, Zebu type (*Bos indicus*) and the remaining 20% are high yielding breeds and their crosses (DLS, 2008). The available genotypes are Holstein-Friesian, Jersey, Sahiwal and their crosses with indigenous cattle. The average predicted 270-day milk yield together with their standard deviations for main breeds, are shown in Table 8.1 (see Chapter 4).

Table 8.1: Estimated lactation milk production (mean ± standard deviation) of available breed groups in Bangladesh

Trait	Genotypes						
	L	S	H	S×L	H× L	J × L	Overall Average
Milk yield (kg)	1697.42 ± 474.01	1738 ± 434.65	2900 ± 365.87	1822.92 ± 502.84	1993.15 ± 629.88	1634.85 ± 383.33	1964.39 ± 465.09

Legends: L = Local, S = Sahiwal, H = Holstein and J = Jersey.

Predicted annual rates of genetic gain for milk yield have been reported to range from 1% to 2% of the mean yield (Powell et al., 1980, and Specht and Mcgilliard, 1960) with the use of artificial insemination and progeny testing. Meuwissen and Woolliams (1993) reported that a 2% annual rate of genetic gain for milk yield was possible, by using an open nucleus breeding scheme. However, in practice, the New Zealand dairy industry achieves one of the highest rates of genetic gain in the world at about 1% of the mean yield per year (LIC, 2008).

To show the degree of genetic change required to meet the national milk requirements in Bangladesh, a sensitivity analysis was carried out using annual rates of genetic gain of 0.25%, 0.50%, 1% and 2% of the mean. These gains were applied to the total milking cow population (10.5 million) assuming an average annual milk yield (1964.39± 465.09 kg, Table 8.1) per cow but with progression of time the cow population will increase and the milk yield from the longer cow population must be added. The growth rate of the dairy cattle population is assumed to be 1.25% and therefore the milking cow population will be 13.5 million after 20 years. On the other hand, after 20 years the human population will be 179 million based on the current growth rate (1.2%, BBS, 2007) and the total milk demand will be increased from 6 to 7.6 million tonnes. At present, the dairy industry of Bangladesh is unorganised, and cow breeding is typically haphazard, suggesting that the present rate of genetic gain is unlikely to be better than 0.25%. Such a rate of genetic gain will not enable Bangladesh to achieve the objective of supplying adequate nutrition for the whole population. The results in Table 8.2 indicate that the annual rate of genetic gain must exceed 1% of the mean in order to meet the deficit in the milk supply in Bangladesh within the next 20 years.

Table 8.2: Sensitivity analysis with various percent of rate of genetic gain (Δg) for milk yield per year per cow, irrespective of breed groups

Trait	Increased MY(kg)/ Cow/ year[1]	Increased MY (million tonnes)/year from current total cow population	Increased milk yield (million tonnes) after 20 years of selection and mating			Total milk yield (million tonnes) after 20 years[2]
			From current total cow population	From increased cow population	Yield from hybrid	
Milk	4.91	0.052	1.03	0.27	0.10	3.56
Yield	9.82	0.103	2.06	0.55	0.10	4.56
(MY)	19.64	0.206	4.12	1.10	0.10	7.47
	39.29	0.413	8.25	2.20	0.10	12.69

[1]Increase in milk yield of ¼%, ½%, 1% and 2%

[2] Assuming current total milk yield = 2.15 million tonnes.

Although crossbreeding enables a more rapid rate of genetic change than can be achieved by selection, it requires considered implementation (Zarate, 1996). The amount of genetic change can be about 2.0% of the mean through the use of crossbreeding (Sørensen et al., 2008). This gain was applied to 15 to 20% of the total milking cow population (1.6 to 2.1 million) assuming an average annual milk yield (1993.15± 629.88kg, Table 8.1) per cow. This figure was obtained from temperate breed (Holstein) crossing, because in Bangladesh the greatest proportion of the crossbred population were Holstein crosses. About 0.064 to 0.10 million tonnes of extra milk can be obtained from a crossbred population per year that is, crossbreds could contribute this extra milk to the national milk yield during next 20 years.

The above calculations show that genetic improvement can assist in improving the quantity of milk produced in Bangladesh. However, to achieve the required genetic gains from the available genotypes in Bangladesh, an effective breeding scheme design with appropriate breeding objectives must be introduced. In addition to the genetic improvement programme, it is also necessary to provide sufficient nutrition, proper management and health care of the dairy animals in order to reach the genetic potential. This thesis has addressed a number of these issues.

8.3 Dairy cattle genetic improvement programme

According to Harris et al. (1984) and Harris and Newman (1994) the following steps should be considered when designing a systematic genetic improvement programme.

1. Describe the production system
2. Set up the objective of the system
3. Choose the breeding systems and breed(s)
4. Estimate selection parameters and economic values
5. Design the animal evaluation system
6. Develop the selection criteria
7. Design the mating system for selected animals
8. Design a system for expansion and
9. Compare alternative programmes

In this thesis steps, 3, 7 and 8 were not considered. The remaining steps were considered and are discussed below.

8.3.1 Description of the production system(s)

To undertake a dairy cattle genetic improvement programme, detailed knowledge on production, and marketing systems, are important. The production and marketing system includes quantifying the number of animals in all classes, herd composition, their feeding and management, replacement policy, total milk, milk products and ages of animals for culling, cull cows and the products for marketing each year. Furthermore, other elements such as the nature of feed, labour, land, buildings and equipment requirements, as well as the corresponding costs of various stages, grazing periods and the lengths of intensive feeding periods (supplementary feeding periods) are also included in the production system.

The dairy production and marketing systems in Bangladesh were discussed in Chapters 3 and 5 of this thesis. In these chapters almost all elements were found, but some other important issues such as the changing pattern of the dairy industry, were not observed. However the consideration of these issues will assist in undertaking a complete programme on genetic improvement.

8.3.2 Objectives of the breeding systems

When designing a genetic improvement programme, the first step is to decide on the breeding objective (Dickerson, 1982 and Goddard, 1998). A breeding objective allows animals to be ranked for a single value, sometimes called an aggregate economic value. The development of a dairy cattle breeding objective must take into account consumers' requirements, farm costs as well as market, manufacturing and genetic information required for the estimation of breeding values.

The decision concerning what traits to improve is ideally based on the extent to which those traits affect profitability per head or per unit and / or change the trait (Ponzoni, 1992 and Baker and Grey, 2003). To achieve the future breeding objectives in genetic improvement programmes of dairy cows under BMPCUL, Bangladesh, traits such as milk yield, fat yield, protein yield, calving intervals, liveweight, birth weight, survivability and calving rate were chosen as traits in the objective, and are studied in Chapter 6 and 7. Similar traits were used by Steine et al. (2008) in the breeding goal for Norwegian Red dairy cattle.

Currently in Bangladesh, payment of milk is based on milk volume, and it is not expected that in future, there is intent to change, and adapt to the New Zealand milk payment system (Milk payment = Price of fat + price of protein – milk carrier) under cooperative dairying in Bangladesh. The economic impact of fat and protein percentage on the direction of genetic improvement proved lower due to the current milk payment system solely based on volume (Chapter 6). However, for future genetic improvement programmes the selection of dairy cattle on the basis of milk, fat and protein yield should be incorporated. Moreover, disease traits were not addressed in the current study, but diseases such as mastitis, parasitic infestation and foot and mouth disease affect dairy farm profits in Bangladesh. These factors should be included in future for the genetic improvement of dairy cattle in Bangladesh, but more research is needed on the economic impact of these traits.

8.3.3 Breeding systems and choice of breeds

This step was not studied in the present thesis. However, crossbreeding studies in Bangladesh were reviewed in Chapter 3. Crossbreeding and straightbreeding were practiced in Bangladesh from 1970, for the improvement of these available dairy cows (Bhuiyan, 1997). Hirooka and Bhuiyan (1995) and Hossain et al. (2002) showed that half-breds of Holstein and local breeds performed better in milk production under improved farming conditions, than purebred Holstein, in Bangladesh. That is, temperate breeds and their crosses produced a higher amount of milk yield than tropical breeds and their crosses. Several authors (e.g. Cunningham and Syrstad, 1987 and Syrstad, 1989) reported similar findings for temperate breeds in a tropical environment. Crossbreeding exploits heterosis, i.e. the superior performance of offspring over the average of the parental breeds, when unrelated individuals are mated, and is due to non-additive genetic effects (Lopez-Villalobos et al., 2000). However, the animal production environment must be able to sustain the crossbred genotypes (Vaccaro, 1990 and Swan and Kinghorn, 1992). Genotype × environment interactions can be very important when introducing crossbreeding programmes. Boettcher et al. (2003) and Kolver et al. (2002) have shown that the genotype × environment interactions in dairy cattle production are important, and they also showed that these interactions can be affect response to selection. Meanwhile, exactly how to produce the hybrid vigour under stressful tropical, Bangladeshi conditions remains in question and more research is needed.

Structured and controlled crossbreeding programmes require considerable infrastructure for management and maintenance of pure breeds to ensure their continuation (Davis and Arthur, 1994). However, several studies (e.g. Hossain et al., 2002) showed that F_1 generation of temperate breed (e.g. Holstein) crosses produce relatively more milk than subsequent generations, and also Deshi cattle. Furthermore, the farmers of the dairy cooperative usually keep the Holstein and its crossbreds for only 2 to 3 lactations, because, after this number of lactations, their productivity and survivability decreases (Chapter 3). This could be due to the breed effects, and also the genotype × environment interactions. Therefore in order to increase milk production. In Bangladesh producing F_1 cows could be the best short-term option. Although low survivability of crossbreds was reported, it is difficult to select on adaptive traits. The adaptability of temperate crossbreds can be less amenable to managerial solutions. Much research is needed to develop suitable selection criteria. Disease problems may be overcome by vaccination, and eradication of parasites or their vectors, although a disease resistance genotype is preferable. Again, more research is needed on this.

8.3.4 Selection parameters and economic values

The selection index is a useful genetic tool in deciding which individuals have the most valuable combination of traits. To derive a selection index, the genetic and phenotypic parameters among the traits and characteristics of interest are needed (Hazel et al., 1994). However, at present such information in Bangladesh is inadequate, although, some is available, albeit being estimated from incomplete data (Hossain et al., 2002). In the development of selection indexes (Chapter 6 and 7), the value of these parameters were taken from other tropical studies, and where those values were not found, assumed values were used. In Bangladesh, there was a shortage of skilled manpower in this field, although nowadays there is some capability for the computation of BLUP EBVs and also estimation of genetic parameters of economically important traits of livestock. For the computation of these parameters, complete records from pedigree and progeny are required, but current recording systems are inadequate. In the future, under BMPCUL, the data recording of both genetic and economic evaluations could be adapted to provide more comprehensive data, since cooperative dairying in Bangladesh is a well developed industry. With more accurate information, genetic and phenotypic parameters could be estimated, and used for the development of individual animal selection indices in the future.

Various authors (e.g. St-Onge et al., 2002 and Kahi and Nitter, 2004) state that profit functions can be used to estimate economic values, which are required to define breeding objectives and predict revenue from breeding programmes. The economic values of traits in the breeding objectives were estimated on a per cow per year basis, and on a per tonne of feed DM basis from the profitability model developed in Chapter 6. Although all the farming factors were considered to develop the model, still more study is needed to incorporate matters such as changing breed composition, feeding, and also the management practices of the dairy industry in Bangladesh.

8.3.5 Develop selection criteria

Due to the unavailability of accurate data in Bangladesh for development of breeding objectives, the values of some selection criteria (e.g. lactation milk yield, fat yield and protein yield) were obtained from fitting lactation curves to data collected from farms providing milk to BMPCUL. The values for other traits were either found from the literature or assumed where those were not available.

Lactation curves derived from mathematical models are an essential research tool for developing and validating production and farm models, for estimating the total lactation yield and explaining the milk production pattern (Macciotta et al., 2005 and Silvestre et al., 2006). In Chapter 4, ten different mathematical models were studied for their predictive ability in describing lactation curves for five different breed groups. Consideration was also given to calving years, seasons and their interaction with breed groups. However, in Chapter 4, issues such as examination of growth curves, the variation of model performance with sampling scheme and properties, the peak yield and the ratio of lactation yield to peak yield, persistency of lactation and other factors like calving age, parity, service period and calving interval were not studied.

Fathi Nasri et al. (2008) described entire lactations by using 6 mathematical equations, comprising four functions (logistic, Gompertz, Schumacher and Morgan) in their differential form with two other equations; Wood and Dijkstra. They observed that the Dijkstra equation was able to estimate the initial milk yield and peak yield more accurately than other equations. Tekerli et al. (2000) measured persistency of lactation yield from the Wood model, the coefficient of variation for monthly test-day yields, and the ratio of lactation yield to peak yield. They also observed that peak and lactation yields were low but persistency was high during the first lactation.

Genetic aspects of lactation curves were not studied in Chapter 4, but they have been addressed by other researchers (e.g. Wood, 1970 and Tekerli et al., 2000). These authors showed that repeatability estimates were moderate for peak (0.26) and lactation (0.34) yields and lower (0.06 to 0.20) for other lactation curve traits. Though recording is inadequate in Bangladesh, genetic improvement programmes require complete data in that situation after fitting the lactation curve, consideration of all the factors should addressed for enabling the national milk requirement to be met. However, more research is needed in this context.

8.3.6 Animal evaluation and comparisons breeding schemes

In Chapters 5 and 6, a linear profitability model was developed based on the relationship between average performance levels for traits related to milk production, and the level of output from the farm using traditional approaches such as Brascamp et al. (1985) and Visscher et al. (1994). The individual cow and farm incomes were estimated. In these chapters, market information on fat and protein yields, and non-market value data on survivability were not accurately kept, and this information is not generally available in Bangladesh. The accurate estimation of farm economics needs rich and reliable data sets with numerous observations. However due to the unavailability of data, assumed values and predicted values obtained from the lactation curve study were used in the simulation study. If a little intervention could be provided to the members of BMPCUL, the data recording in both the genetic and economic evaluations could be adapted to provide more comprehensive data in the future as cooperative dairying in Bangladesh is already well developed.

Several authors (e.g. Da and Grossman, 1991; Albuquerque et al., 1996 and Demeke et al., 2004) have been obtain genetic evaluations of economically important traits of dairy cattle. In Chapter 7, the estimated breeding values (EBVs) were obtained from univariate and multivariate analyses, based on restricted maximum likelihood using the average information matrix as second derivatives in a quasi-Newton procedure

(Johnson and Thompson, 1995). This method calculated second derivatives from the average of observed and expected values, which provide an efficient and simple computing algorithm for variance component estimation of an animal model. Therefore, this method has been prefered for estimation of variance components and EBVs.

The individual cow performance for yields of milk, fat and protein, liveweight and longevity were simulated by using a stochastic approach to evaluate the two breeding schemes (progeny testing and parent-average breeding scheme) and three selection objectives (milk merit, milk & survivability merit and total merit) in Chapter 7. The additive genetic merit of bulls and cows was considered under straightbreeding in this simulation, and the genetic gains of the individual traits were derived from the regression of the economic merit index of the whole population. In this simulation, the nucleus breeding scheme, and the combination of selection and crossbreeding was not considered. However, James (1977 and Kahi et al. (2004) reported that higher rates of genetic gain using straightbreeding was obtained in an open nucleus breeding scheme, compared with an unstructured industry. Furthermore, a higher rate of genetic gain was reported by using either crossbreeding (Zarate, 1996) or a combination of selection and crossbreeding (Lopez-Villalobos et al. 2000). A further study is recommended to evaluate the breeding schemes with the objective of improving the milk, milk & survival and total merit of progeny considering both additive and non-additive effects by using selection and crossbreeding according to Kinghorn (1992) and Hayes and Visscher (1998).

8.4. Functional traits

Functional traits such as fertility, longevity, resistance to mastitis and other diseases are important in dairy cattle breeding (Dematawewa and Berger, 1998; Essl, 1998 and Gonzalez-Recio and Alenda, 2005). However, these traits often have low heritabilities resulting in low EBV accuracy for cows and young bulls. Cows with poorer fertility and longevity are generally culled involuntarily from the herd (Wall et al., 2003) leading to increased farm profitability. However, culling poorly performing cows will have little impact on the average genetic merit of the herd for these traits.

Fertility problems can also be reduced by improving feeding, management and better heat detection. Direct selection on fertility would also improve milk yield (Royal et al., 2002). The genetic merit of fertility traits (calving interval and insemination data) can be predicted by measures of recorded correlated traits (VeerKamp et al., 2001 and Wall et al., 2003).

Traits such as disease incidence, dystocia, poor reproductive performance and severe conformation deficiencies, are important determinants and affect longevity (Essl, 1998). Thus selection based on such determinants, primarily reduce the incidence of involuntary culling, which simultaneously increases the genetic potential of longevity. Longevity or length of productive life is an important trait affecting dairy farm profitability (Madgwick and Goddard., 1989). When designing a genetic improvement programme functional traits such as fertility and longevity should be incorporated as selection criteria for increasing milk production in future in order to meet the national demand for milk and milk products.

8.5. Main findings and recommendations

- In Bangladesh there is a shortage of milk and milk products and this demand could be met by achieving an annual rate of genetic gain of at least 1% of the mean. To achieve this response, a properly designed genetic improvement programme should be set up for consideration of all of the aspects of a breeding scheme.

- In the study of lactation curves, breeding objectives and selection indexes, some parameters were either inadequately reported or unavailable. This required that some values be either assumed, or sourced from other tropical studies. Future research should aim to estimate these values.

- In the multitrait stochastic simulation and evaluation of breeding schemes studied, it was found that both the progeny testing and parent-average breeding schemes could improve on the current rate of genetic gains and improve farm profitability.

- Genetic improvement is a viable strategy to help increase the profit for dairy farming, and to alleviate poverty, increase food security and enhance sustainable agriculture in Bangladesh.

- To obtain the full benefits from genetic improvement, simultaneous improvement in the environment (e.g. nutrition, husbandry, marketing and policy) is also vital.

- The design of a breeding programme, will depend on the amount of recording, and the degree of genetic gain aimed for, and also the number of improved animals required for dissemination (Cunningham, 1981 and Zarate, 1996). It is helpful for animal breeding improvement programmes, after identification of a suitable breed(s) in a particular production and marketing system, to work within a cooperative approach, which facilitates data recording, and can compute individual breeding values for traits considered important, using information on relationship and genetic parameters appropriate for the production system.

Recommendations for future research on dairy cattle genetic improvement in Bangladesh are:

1. That research on the genetic improvement of dairy cattle uses test-day models to improve the accuracy and heritability of production proofs; test-day models also allow the evaluation of persistency of lactation.

2. In Bangladesh, only limited research has been undertaken on estimating the genetic merit of available genotypes, economic evaluations of different breeds in different management schemes, and genetic improvement programmes of dairy cattle. Additional research should be started immediately, by investing in long-term programmes which will also enable the development of more manpower within these important disciplines.

3. It would be possible to adapt an Open Nucleus Breeding System (ONBS) for implementation by BMPCUL. The Animal Breeding Section at Baghabarighat milk shed area could host a nucleus herd with intensive recording and selection of herds from cooperative farmer member's being used for commercial production of milk. Both progeny testing and parent-average testing schemes could be adapted through ONBS by using artificial insemination. In the near future, multiple ovulation and embryo transfer (MOET), marker assisted selection (MAS) and genomic selection approaches could be considered for introduction, with ONBS for rapid genetic improvement of dairy cattle.

4. A systematic crossbreeding programme could be introduced to retain heterosis and to ensure breed complementarity. However, additional research on the estimation of additive differences of indigenous, tropical and temperate breeds and genotype × environment interactions as well as the percentage of heterosis that would be sustained is needed.

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APPENDIX ONE

Production, processing and Marketing systems of cooperative dairying in Bangladesh

A. 1. 1. Production, processing and Marketing systems of cooperative dairying in Bangladesh

Objectives: To investigate the present production, processing and marketing systems of cooperative dairying in Bangladesh.

Farm code no: -----------------------------------

1. a) Name of owner: ---
-
Age :------- ----------------------   Level of education:---------------------------

   b) Address:
   Village/Road:----------------------Upazilla:------------------District:--------------

   c) Occupation: ----------------------   d) Yearly income:-----------------------------

2. Total land: ---------------- a) Cultivable------------------b)Area of farm:---------------
-
   c) Area for fodder production:--

3. Types and Number of cattle:

Breed/Variety	ID No.	Calve (s)	Heifer (s)	Bull calve	Cow(s)								Bull -ock	Total
					4	5	6	7	8	9	10			
Pure breed														
Indigenous														
Pabna Cattle														
Holstein-Friesian														
Sahiwal														
Red-Sindhi														
Crossbred														
Pabna × Local(F_1)														
Pabna × Local (F_2)														
Sahiwal × Pabna (F_1)														
Sahiwal × Pabna(F_2)														
Pabna × Sahiwal (F_1)														
Pabna × Sahiwal (F_2)														
Sahiwal × Local (F_1)														
Sahiwal × Local (F_2)														
Local × Sahiwal (F_1)														
Local × Sahiwal (F_2)														
Shindhi × Local (F_1)														
Shindhi × Local (F_2)														
Local × Shindhi (F_1)														
Local × Shindhi(F_2)														
Shindhi × Pabna(F_1)														
Shindhi × Pabna (F_2)														

Pabna × Shindhi (F_1)														
Pabna × Shindhi (F_2)														
Holstein × Sahiwal (F_1)														
Holstein × Sahiwal (F_2)														
Sahiwal × Holstein (F_1)														
Sahiwal × Holstein (F_2)														
Holstein × Local (F_1)														
Holstein ×Local (F_2)														
Local × Holstein (F_1)														
Local × Holstein (F_2)														
Holstein × Pabna (F_1)														
Holstein × Pabna (F_2)														
Pabna× Holstein (F_1)														
Pabna × Holstein (F_2)														
Grand total														
Live weight														
Average live weight														

4. Availability of feeds and fodders throughout the year:

Types of feed	Mar.-May (Summer)	Jun.-Aug. (Monsoon)	Sep.-Nov. (Autumn)	Dec- Feb. (Winter)
Straw				
Green grass				
Natural pasture				
Concentrate				
Silage				
Hay				
Others				

5. Feed Ingredients:

a) Roughages (i) (ii) (iii) (iv)

(v) (vi) (vii)

b) Concentrates (i) (ii) (iii) (iv)
(v) (vi)

6. Amount of feed consumption per day and the price of consumed feed:

Genotypes	**Id No**	Roughages												Concentrate											
		Calve(s)		Heifer (s)		Yearling bull(s)		Cow(s)		Bull(s)		Bullock (s)		Calve (s)		Heifer(s)		Yearling bull(s)		Cow(s)		Bull(s)		Bull -ock(s	
		Kg	*t*	Kg	*t*	Kg	*t*	Kg	*t*	Kg	*t*	Kg	*t*	Kg	*t*	Kg	*t*	Kg	*t*	Kg	*t*	Kg	*t*	Kg	*t*
Purebreed																									
Indigenous																									
Pabna Cattle																									
Holstein-Friesian																									
Sahiwal																									
Red-Sindhi																									
Crossbred																									
Pab × L(F_1)																									
Pab× L (F_2)																									
S × Pab (F_1)																									
S × Pab(F_2)																									
Pab × S (F_1)																									
Pab × S (F_2)																									
S × L (F_1)																									
S × L (F_2)																									
L × S (F_1)																									
L × S (F_2)																									
RS × L (F_1)																									
RS × L (F_2)																									
L × RS (F_1)																									
L × RS(F_2)																									
RS × Pab (F_1)																									
RS × Pab (F_2)																									
Pab × RS (F_1)																									
Pab × RS (F_2)																									
HF × S (F_2)																									
S × HF (F_1)																									
S × HF (F_2)																									
HF × L (F_1)																									
HF ×L (F_2)																									
L × HF (F_1)																									
L × HF (F_2)																									
HF × Pab (F_1)																									
HF × Pab (F_2)																									
Pab× HF (F_1)																									
Pab× HF (F_2)																									
Grand total																									

L= Local, S= Sahiwal, RS= Red Shindhi, Pab= Pabna, HF= Holstein Friesian.

7. Live weight:

Genotypes	Sir Id No	Dam Id No	Ind. ID No	Birth wt (kg)		Weaning wt (Kg)		Weight at puberty	Mature LWT	Bulls LWT	Bullock LWT
				M	F	M	F	Kg	Kg	Kg	Kg
Purebreed											
Indigenous											
Pabna Cattle											
Holstein											
Sahiwal											
Red-Sindhi											
Crossbred											
Pabna × Local(F_1)											
Pabna × Local (F_2)											
Sahiwal × Pabna (F_1)											
Sahiwal × Pabna(F_2)											
Pabna × Sahiwal (F_1)											
Pabna × Sahiwal (F_2)											
Sahiwal × Local (F_1)											
Sahiwal × Local (F_2)											
Local × Sahiwal (F_1)											
Local × Sahiwal (F_2)											
Shindhi × Local (F_1)											
Shindhi × Local (F_2)											
Local × Shindhi (F_1)											
Local × Shindhi(F_2)											
Shindhi × Pabna(F_1)											
Shindhi × Pabna (F_2)											
Pabna × Shindhi (F_1)											
Pabna × Shindhi (F_2)											
Holstein × Sahiwal (F_1)											
Holstein × Sahiwal (F_2)											
Sahiwal × Holstein (F_1)											
Sahiwal × Holstein (F_2)											
Holstein × Local (F_1)											
Holstein ×Local (F_2)											
Local × Holstein (F_1)											
Local × Holstein (F_2)											
Holstein × Pabna (F_1)											
Holstein × Pabna (F_2)											
Pabna× Holstein (F_1)											
Pabna × Holstein (F_2)											

8. Reproductive characteristics of different genotypes:

Genotypes	Sire ID No	Dam Id No	Ind. Id No	Age at sexual maturity	Calving Interval (days)	Gestation length (day)	Post partum heat (day)	Service per conception	Calving percent
Purebreed									
Indigenous									
Pabna Cattle									
Holstein									
Sahiwal									
Red-Sindhi									
Crossbred									
Pabna × Local(F_1)									
Pabna × Local (F_2)									
Sahiwal × Pabna (F_1)									
Sahiwal × Pabna(F_2)									
Pabna × Sahiwal (F_1)									
Pabna × Sahiwal (F_2)									
Sahiwal × Local (F_1)									
Sahiwal × Local (F_2)									
Local × Sahiwal (F_1)									
Local × Sahiwal (F_2)									
Shindhi × Local (F_1)									
Shindhi × Local (F_2)									
Local × Shindhi (F_1)									
Local × Shindhi(F_2)									
Shindhi × Pabna(F_1)									
Shindhi × Pabna (F_2)									
Pabna × Shindhi (F_1)									
Pabna × Shindhi (F_2)									
Holstein × Sahiwal (F_1)									
Holstein × Sahiwal (F_2)									
Sahiwal × Holstein (F_1)									
Sahiwal × Holstein (F_2)									
Holstein × Local (F_1)									
Holstein ×Local (F_2)									
Local × Holstein (F_1)									
Local × Holstein (F_2)									
Holstein × Pabna (F_1)									
Holstein × Pabna (F_2)									
Pabna× Holstein (F_1)									
Pabna × Holstein (F_2)									

9. Milk production characteristics of different genotypes:

Genotypes	Sire ID NO	Dam ID No	Inv. ID NO	Daily milk yield (kg)	Lactati on length	Total milk yield (Kg)	Total Solid (Kg)	Total Fat (Kg)	Total Protein (Kg)	Lactation number
Purebreed										
Indigenous										
Pabna Cattle										
Holstein										
Sahiwal										
Red-Sindhi										
Crossbred										
Pabna × Local(F_1)										
Pabna × Local (F_2)										
Sahiwal × Pabna (F_1)										
Sahiwal × Pabna(F_2)										
Pabna × Sahiwal (F_1)										
Pabna × Sahiwal (F_2)										
Sahiwal × Local (F_1)										
Sahiwal × Local (F_2)										
Local × Sahiwal (F_1)										
Local × Sahiwal (F_2)										
Shindhi × Local (F_1)										
Shindhi × Local (F_2)										
Local × Shindhi (F_1)										
Local × Shindhi(F_2)										
Shindhi × Pabna(F_1)										
Shindhi × Pabna (F_2)										
Pabna × Shindhi (F_1)										
Pabna × Shindhi (F_2)										
Holstein × Sahiwal (F_1)										
Holstein × Sahiwal (F_2)										
Sahiwal × Holstein (F_1)										
Sahiwal × Holstein (F_2)										
Holstein × Local (F_1)										
Holstein × Local (F_2)										
Local × Holstein (F_1)										
Local × Holstein (F_2)										
Holstein × Pabna (F_1)										
Holstein × Pabna (F_2)										
Pabna× Holstein (F_1)										
Pabna × Holstein (F_2)										

10. Survivability of different genotype:

Genotypes	Calve (s)		Heifer(s)		Cow(s)		Yearling Bull (s)		Bull(s)		Bullock(s)		Reason for culling	Ave. No of Lac/ cow
	Total	No. alive	Total	No alive	Total	No alive	Total	No alive	Total	No alive	Total	No alive		
Purebreed														
Indigenous														
Pabna Cattle														
Holstein														
Sahiwal														
Red-Sindhi														
Crossbred														
Pabna × Local(F_1)														
Pabna × Local (F_2)														
Sahiwal × Pabna (F_1)														
Sahiwal × Pabna(F_2)														
Pabna × Sahiwal (F_1)														
Pabna × Sahiwal (F_2)														
Sahiwal × Local (F_1)														
Sahiwal × Local (F_2)														
Local × Sahiwal (F_1)														
Local × Sahiwal (F_2)														
Shindhi × Local (F_1)														
Shindhi × Local (F_2)														
Local × Shindhi (F_1)														
Local × Shindhi(F_2)														
Shindhi × Pabna(F_1)														
Shindhi × Pabna (F_2)														
Pabna × Shindhi (F_1)														
Pabna × Shindhi (F_2)														
Holstein × Sahiwal (F_1)														
Holstein × Sahiwal (F_2)														
Sahiwal × Holstein (F_1)														
Sahiwal × Holstein (F_2)														
Holstein × Local (F_1)														
Holstein ×Local (F_2)														
Local × Holstein (F_1)														
Local × Holstein (F_2)														
Holstein × Pabna (F_1)														
Holstein × Pabna (F_2)														
Pabna× Holstein (F_1)														
Pabna × Holstein (F_2)														

11. Diseases:

Genotypes	Sire ID NO	Dam Id No	Ind. Id No	Calve(s)	Heifer (s)	Cow(s)	Yearling Bull(s)	Bull(s)	Bullock(s)	Treament cost (taka)
Purebreed										
Indigenous										
Pabna Cattle										
Holstein										
Sahiwal										
Red-Sindhi										
Crossbred										
Pabna × Local(F_1)										
Pabna × Local (F_2)										
Sahiwal × Pabna (F_1)										
Sahiwal × Pabna(F_2)										
Pabna × Sahiwal (F_1)										
Pabna × Sahiwal (F_2)										
Sahiwal × Local (F_1)										
Sahiwal × Local (F_2)										
Local × Sahiwal (F_1)										
Local × Sahiwal (F_2)										
Shindhi × Local (F_1)										
Shindhi × Local (F_2)										
Local × Shindhi (F_1)										
Local × Shindhi(F_2)										
Shindhi × Pabna(F_1)										
Shindhi × Pabna (F_2)										
Pabna × Shindhi (F_1)										
Pabna × Shindhi (F_2)										
Holstein × Sahiwal (F_1)										
Holstein × Sahiwal (F_2)										
Sahiwal × Holstein (F_1)										
Sahiwal × Holstein (F_2)										
Holstein × Local (F_1)										
Holstein ×Local (F_2)										
Local × Holstein (F_1)										
Local × Holstein (F_2)										
Holstein × Pabna (F_1)										
Holstein × Pabna (F_2)										
Pabna× Holstein (F_1)										
Pabna × Holstein (F_2)										

12. Vaccination

a) Regular Vaccination: ------------------------------ Yes/ No
b) Name the vaccines: ---
c) Cost of vaccine/animal:---
d) Cost of dewarming/animal:--

13. Breeding:
    a) Artificial insemination/ natural :---
    b) Which genotype you preferred:---
    Why:---

14. Feed processing /conservation: Silage/hay--
    a) Amount of conserved fodder ---
    b) Area of conservation---

15. Processing of milk:

Product	Price/kg milk (*taka*)	Lmilk/Kg product (*taka)*	Price/kg product (*taka)*	Income (*taka)*
Raw milk				
Pasteurized milk				
Yoghurt/dahi				
Butter				
Cheese				
Sweatmeat				
Icecream				
Chocolate				
Meat				

16. Marketing: --
----

17. Labour:

Number of cattle	Required number of labour	Number of labour for feed & fodder cultivation	Number of labour involved in milking	Number of labour involved in feed conservation	Number of labour involved in marketing	Cost per labour/day

18. Machineries for farm operation:

Sl. No.	Permanent	Temporary	Cost
Total cost			

19. Income
    a) Milk income/cow:--
    b) Milk income/ farm:--
    c) Manure sale proceed/ farm /year:--
    d) Manure sale proceed/cow/year :---
    e) Cull cows/year:--
    f) Surplus cow/ year:--
    g) Surplus Heifer/year:--
    h) Bull calves/year:---
    i) Draught/year:---
    j) Gunny bags/year:---

20. Expenses:

A) Capital Investment:
    a) Land:---
    b) House:---
    c) Equipments:--
    d) Animal purchase: ---

B) Recurrent expenditure:
    a) Feed cost
        (i) Roughage/cow:---
        (ii) Roughage/year:---
        (iii) Concentrate/cow:--
        (iv) Concentrate/year:--
    b) Treatment cost/ animal:---
    c) Treatment cost/ farm:---
    d) Vaccination cost/ cow:---
    e) Vaccination cost/ farm:--
    f) Labour cost/ cow:--
    g) Marketing cost/ year:---
    h) Feeds and fodder cultivation costs: --------------------------------------
    i) Insemination cost/ cow:---
    j) Insemination cost/ year:--

C) Non Dairy
    a) Depreciation cost:--
    b) Bank interest: --
    c) Repair and maintenance costs: --
    d) Others: ---

21. List the problems for dairy cattle rearing and general opinion for the improvement
of dairy cattle production in Bangladesh:
    a) Problems
        1.
        2.
        3.
        4.
    b) Opinion
        1.
        2.
        3.

A.1.2. Individual cow performance

Objective: To estimate the genotypic and phenotypic parameters.

a) Reproductive performance

Cow ID No	Sire	Dam	Farm Code	Breed Composition					DOB	Birth Wt	DFM	S/C	DOC	CI	Parity	Remarks
				L	P	HF	S	RS								

Legends: L= Local; P= Pabna; HF= Holstein Friesian; S= Sahiwal; RS= Red-Sindhi, DOB= Date of birth; DFM= Date of first mating; S/C= Service per conception; DOC= Date of first calving; CI= Calving interval.

b) Milk production performance

Cow ID No	Sire	Dam	Farm Code	Breed Composition					DMY	TS	TF	TP	LL	TLP	PLN	TL	DoC	Reasons for culling
				L	P	HF	S	RS										

Legends: DMY= Daily milk yield; TS=Total solids; TF=Total fat; TP=Total protein; LL=Lactation length; TLP=Total lactation production; PLN=Present lactation number; TL=Total Lactation; DoC= Date of Culling;

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APPENDIX TWO (A)

The effects of calving years (1999 to 2001), seasons (dry and wet) and their interactions with different genotypes on the parameters of ten different mathematical models, goodness of fit (AIC, R^2, CCC and RMSPE) statistics and the predicted milk yields

Table A 2.1: Least square means (±SE) of different parameters (a, b, c, d and k), fit statistics and predicted milk yield for the Gaines model

Effects			Model parameters		Fit statistics				Predicted milk yield
			a	b	R^2	AIC	RootMSPE	CCC	
Effects of years	1999		2.10±0.02	-0.0009^{xy}±0.0001	0.54±0.022	59.61±0.49	0.17±0.005	0.66±0.02	1597.72^{y}±42.68
	2000		2.04±0.02	-0.0013^{y}±0.0003	0.51±0.02	58.83±0.37	0.17±0.004	0.68±0.02	1696.34^{xy} ±32.17
	2001		2.06±0.05	-0.0004^{x}±0.0003	0.56±0.05	59.20±1.05	0.16±0.01	0.67±0.05	1886.74^{x}±90.68
Effects of season	1		2.06±0.02	-0.0027±0.0002	0.60±0.02	58.59±0.60	0.18±0.006	0.67±0.02	1596.66^{y}±35.97
	2		2.06±0.02	-0.0021±0.0001	0.50±0.02	59.37±0.45	0.16±0.005	0.68±0.02	1747.16^{x}±34.77
Effects of seasons × breeds	A × P	1	2.12±0.06	-0.0024^{xy}±0.0003	0.60±0.05	60.08±1.22	0.14±0.01	0.63^{y}±0.05	1807.77^{x}±105.02
		2	2.25±0.07	-0.0026^{xy}±0.0004	0.55±0.06	62.13±1.42	0.15±0.02	0.60^{y}±0.06	1941.86^{x}±122.86
	H × P	1	2.15±0.03	-0.0026^{xy}±0.0001	0.64±0.03	60.80±0.60	0.15±0.006	0.66^{xy}±0.03	1821.25^{x}±52.02
		2	2.13±0.03	-0.0020^{y}±0.0002	0.48±0.02	60.56±0.55	0.17±0.006	0.68^{xy}±0.02	1922.43^{x}±47.33
	J × P	1	1.90±0.13	-0.0029^{x}±0.0007	0.48±0.11	54.93±2.53	0.20±0.03	0.84^{x}±0.11	1312.63^{y}±218.63
		2	1.89±0.07	-0.0017^{y}±0.0004	0.43±0.06	57.14±1.39	0.16±0.01	0.72^{x}±0.06	1618.15^{y}±119.75
	P	1	2.01±0.03	-0.0032^{x}±0.0002	0.67±0.03	57.97±0.64	0.17±0.007	0.66^{xy}±0.03	1398.06^{y}±55.53
		2	1.96±0.04	-0.0022^{xy}±0.0002	0.49±0.03	57.53±0.75	0.17± 0.008	0.67^{xy}±0.03	1571.18^{y}±64.94
	S × P	1	2.08±0.03	-0.0028^{x}±0.0001	0.58±0.02	59.18±0.52	0.18±0.006	0.67^{xy}±0.02	1538.65^{y}±44.78
		2	2.11±0.03	-0.0022^{xy}±0.0002	0.56±0.02	59.47±0.55	0.17±0.006	0.69^{xy}±0.02	1710.31^{xy}±47.15
Effects of breeds × years	A × P	1999	2.38^{x}±0.09	-0.004±0.0005	0.80^{x} ±0.08	64.18±1.71	0.15±0.02	0.72^{x}±0.07	1961.78^{x}±148.11
		2000	2.09^{xy}±0.05	-0.002±0.0003	0.49^{y}±0.05	59.63±1.09	0.15±0.01	0.66^{xy}±0.05	1824.82^{xy}±94.40
	H × P	1999	2.15^{x}±0.04	-0.0029±0.0003	0.67^{x}±0.04	60.73±0.87	0.16±0.009	0.62^{xy}±0.04	1734.73^{xy}±75.52
		2000	2.13^{x}±0.02	-0.0022±0.0001	0.51^{y}±0.02	60.57±0.49	0.16±0.005	0.67^{xy}±0.02	1876.81^{x}±41.96
		2001	2.15^{x}±0.07	-0.002±0.0004	0.62^{xy}±0.06	61.31±1.32	0.16±0.01	0.70^{x}±0.06	2197.43^{x}±113.85
	J × P	1999	2.15^{x}±0.14	-0.0025±0.0008	0.63^{xy}±0.12	60.96±2.76	0.16±0.03	0.88^{x}±0.12	1773.71^{xy}±238.82
		2000	1.83^{y}±0.07	-0.0018±0.0004	0.40^{y}±0.06	55.60±1.35	0.19±0.01	0.68^{xy}±0.06	1493.82^{y}±116.53
	P	1999	2.04^{xy}±0.04	-0.0036±0.0002	0.70^{x}±0.04	58.60±0.82	0.17±0.009	0.65^{xy}±0.04	1389.13^{y}±70.73
		2000	1.96^{y}±0.03	-0.0023±0.0002	0.53^{y}±0.03	57.45±0.63	0.17±0.007	0.66^{xy}±0.03	1524.83^{y}±54.50
		2001	1.88^{y}±0.12	-0.0026±0.0007	0.65^{x}±0.11	55.11±2.34	0.15±0.03	0.66^{xy}±0.1	1284.01^{y}±201.84
	S × P	1999	2.11^{x}±0.03	-0.0030±0.0002	0.61^{xy}±0.03	59.32±0.62	0.18±0.007	0.71^{x}±0.06	1540.16^{y}±53.14
		2000	2.08^{xy} ±0.02	-0.0023±0.0001	0.55^{y}±0.02	59.26±0.49	0.17±0.005	0.68^{x}±0.02	1656.56^{y}±42.09
		2001	2.13^{x}±0.09	-0.0021±0.0006	0.64^{x}±0.09	60.27±1.95	0.17±0.02	0.55^{y}±0.09	1839.50^{xy}±168.87

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination; RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at $P < 5\%$.

Table A 2.2: Least square means (±SE) of different parameters (a, b, c, d and k) , fit statistics and predicted milk yield for the Wood model

Effects			Model parameters			Fit statistics				Predicted milk yield
			a	b	c	AIC	R^2	CCC	RootMSPE	
Effects of years	1999		1.28±0.05	0.25±0.01	-0.0054±0.0002	67.94±0.64	0.54 ±0.02	0.87±0.01	0.24±0.08	1610.37^{y}±39.85
	2000		1.20±0.04	0.27±0.01	-0.0052±0.0001	67.74±0.48	0.52±0.01	0.88±0.01	0.23±0.06	1661.33^{xy}±29.99
	2001		1.23±0.11	0.27±0.03	-0.0052±0.0004	67.60±1.35	0.54 ± 0.04	0.89±0.02	0.23±0.02	1787.74^{x}±84.71
Effects of season	1		1.27^{x}±0.04	0.19^{y}±0.01	-0.0054±0.0002	67.73±0.77	0.54±0.02	0.87±0.01	0.24±0.010	1625.69±33.61
	2		1.02^{y}±0.04	0.28^{x}±0.01	-0.0054±0.0002	67.77±0.57	0.51±0.02	0.88±0.01	0.23±0.007	1674.32±32.54
Effects of seasons × breeds	A × P	1	1.55^{x}±0.12	0.18^{y}±0.04	-0.0053±0.0004	67.57±1.56	0.53^{xy}±0.05	0.88±0.02	0.23^{x}±0.64	1686.27^{xy}±98.29
		2	1.19^{xy}±0.14	0.30^{x}±0.04	-0.0058±0.0005	68.77±1.78	0.56^{x}±0.06	0.89±0.03	0.24^{xy}±0.48	1868.71^{x}±112.08
	H × P	1	1.28^{x}±0.06	0.27^{xy}±0.02	-0.0054±0.0002	67.97±0.76	0.57^{x}±0.02	0.88±0.01	0.21^{x}±0.01	1799.14^{x}±48.01
		2	1.07^{xy}±0.06	0.32^{x}±0.02	0.0056±0.0002	68.34±0.71	0.54^{xy}±0.02	0.88±0.01	0.21^{x}±0.09	1808.55^{x}±44.83
	J × P	1	0.88^{y}±0.26	0.35^{x}±0.07	-0.0067±0.0009	66.87±3.25	0.47^{y}±0.1	0.80±0.05	0.30^{y}±0.04	1344.11^{y}±204.62
		2	1.14^{xy}±0.14	0.27^{xy}±0.04	-0.0050±0.005	67.73±1.78	0.40^{y}±0.06	0.89±0.03	0.27^{y}±0.02	1631.19^{y}±112.08
	P	1	1.43^{x}±0.07	0.19^{y}±0.02	-0.0049±0.0002	66.91±0.82	0.55^{xy}±0.03	0.87±0.01	0.23^{x}±0.02	1542.79^{y}±51.97
		2	1.08^{xy}±0.08	0.28^{xy}±0.02	-0.0053±0.0003	67.31±0.97	0.48^{y}±0.03	0.87±0.01	0.24^{xy}±0.01	1528.09^{y}±61.23
	S × P	1	1.09^{xy}±0.05	0.30^{x}±0.01	-0.0057±0.0002	69.33±0.66	0.59^{x}±0.02	0.89±0.01	0.20^{x}±0.08	1547.08^{y}±41.77
		2	1.26^{x}±0.06	0.26^{xy}±0.02	-0.0052±0.0002	66.72±0.70	0.54^{xy}±0.02	0.89±0.01	0.21^{x}±0.09	1627.29^{y}±44.30
Effects of breeds × years	A × P	1999	1.67^{x}±0.17	0.18^{y}±0.04	-0.0049^{y}±0.0006	68.28±2.14	0.63^{x}±0.07	0.88^{xy}±0.03	0.21^{x}±0.03	1985.00^{x}±133.20
		2000	1.27^{x}±0.37	0.25^{xy}±0.03	-0.0049^{y}±0.0004	67.57±1.41	0.51^{y} ±0.04	0.89^{x}±0.02	0.24^{xy}±0.02	1669.60^{xy}±88.10
	H × P	1999	1.25^{x}±0.09	0.27^{xy}±0.03	0.0054^{xy}±0.0003	68.34±1.14	0.51^{y}±0.04	0.88^{xy}±0.02	0.24^{xy}±0.01	1730.73^{xy}±71.19
		2000	1.12^{xy}±0.05	0.31^{x}±0.01	-0.0055^{xy}±0.0002	68.10±0.63	0.57^{xy}±0.02	0.88^{xy}±0.01	0.20^{x}±0.07	1798.04^{xy}±39.04
		2001	1.32^{xy}±0.14	0.26^{xy}±0.04	-0.005^{y}±0.0004	68.25±1.71	0.54^{xy} ±0.05	0.89^{x}±0.02	0.21^{x}±0.02	2013.10^{x}±106.25
	J × P	1999	1.25^{xy}±0.28	0.28^{xy}±0.08	-0.0055^{xy}±0.0009	69.80±3.58	0.40^{y} ±0.11	0.79^{y}±0.05	0.31^{y}±0.04	1858.75^{xy}±222.88
		2000	1.04^{xy}±0.15	0.29^{xy}±0.04	-0.0054^{xy}±0.0005	66.99±1.75	0.42^{y}±0.05	0.89^{x}±0.03	0.27^{y}±0.02	1495.99^{y}±108.75
	P	1999	1.52^{x}±0.08	0.17^{y}±0.02	-0.0049^{y}±0.0003	67.16±1.07	0.56^{xy}±0.03	0.85^{y}±0.02	0.23^{xy}±0.01	1450.00^{x}±66.59
		2000	1.14^{xy}±0.06	0.27^{xy}±0.02	-0.0051^{y}±0.0002	67.06±0.81	0.50^{y}±0.03	0.88^{xy}±0.01	0.23^{xy}±0.01	1593.09±50.60
		2001	1.31^{xy}±0.24	0.22^{x}±0.07	-0.0051^{y}±0.0008	66.64±3.02	0.42^{y} ±0.09	0.87^{xy}±0.04	0.29^{y}±0.04	1447.33^{y}±188.37
	S × P	1999	1.07^{xy}±0.06	0.31^{x}±0.02	-0.0059^{xy}±0.0002	68.02±0.80	0.59^{xy}±0.02	0.88^{xy}±0.01	0.21^{x}±0.010	1532.81^{y}±49.84
		2000	1.25^{x}±0.05	0.26^{xy}±0.01	-0.0051^{y}±0.0002	68.19±0.63	0.55^{xy} ±0.02	0.89^{x}±0.01	0.21^{x}±0.008	1609.78^{xy}±39.16
		2001	0.85^{y}±0.20	0.39^{x}±0.06	-0.0063^{x}±0.0007	67.50±2.53	0.73^{x}±0.08	0.93^{x}±0.04	0.15^{x}±0.03	1700.72^{xy}±157.60

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination; RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at $P < 5\%$.

Table A 2.3: Least square means (±SE) of different parameters (a, b, c, d and k), fit statistics and predicted milk yield for the Polynomial model

Effects			Model parameters					Fit statistics				Predicted milk yield
			a	b	c	d	k	R^2	AIC	RootMSPE	CCC	
Effects of years		1999	6.49±0.46	0.078±0.02	-0.0012±0.0002	6.09E-6^{y}±1.3E-6	-1.05E-8	0.70±0.06	42.25±0.58	0.61±0.08	0.86±0.01	1581.60 ±35.47
		2000	6.44±0.46	0.067±0.02	-0.0009±0.0002	4.38E-6^{x}±1.28E-6	-7.2E-9	0.67±0.06	40.18±0.44	0.64±0.06	0.86±0.01	1649.34±26.63
		2001	6.54±0.55	0.075±0.02	-0.0010±0.0003	4.71E-6^{x}±1.54E-6	-7.63E-9	0.65±0.07	42.10±1.22	0.59±0.17	0.88±0.01	1735.13±76.01
Effects of Seasons		1	6.53±0.45	0.070±0.02	-0.0011±0.0002	5.218E-6	-8.83E-9	0.69±0.06	41.89±0.71	0.61±0.07	0.87±0.01	1595.21±42.77
		2	6.38±0.46	0.073±0.02	-0.0010±0.0002	4.762E-6	-7.86E-9	0.64±0.06	40.32±0.53	0.65±0.06	0.87±0.01	1661.93±32.15
Effects of Seasons × breeds	A × P	1	6.52^{x}±0.41	0.101±0.01	-0.0016±0.0002	7.681E-6 ± 1.161E-6	1.27E-8	0.57±0.05	40.89^{xy}±1.44	0.64±0.19	0.92^{x} ±0.03	1755.83^{x}± 87.01
		2	5.73^{y}±0.46	0.117±0.02	-0.0016±0.0002	7.698E-6±1.324E-6	-1.24E-8	0.57±0.06	42.67^{y}±1.65	0.54±0.21	0.89^{x} ±0.03	1728.39^{xy}±99.21
	H × P	1	6.25^{x}±0.20	0.084±0.007	-0.0012±0.0001	5.53E-6	-9.17E-9	0.59±0.03	41.87^{xy}±0.71	0.59±0.10	0.85^{xy} ±0.01	1722.85^{xy}±42.49
		2	5.65^{y}±0.19	0.101±0.007	-0.0013±0.0001	5.35E-6	-8.12E-9	0.56±0.02	41.14^{xy}±0.66	0.66±0.09	0.88^{xy} ±0.01	1803.07^{x} ±39.68
	J × P	1	5.27^{y}±0.85	0.06^{y}±0.031	-0.0006±0.0004	8.17E-7±2.42E-6	1.5E-9	0.55±0.11	43.15^{y}±3.01	0.69±0.39	0.90^{x} ±0.06	1458.43±181.12
		2	5.58^{y}±0.46	0.080±0.02	-0.0011±0.0002	5.34E-6±1.32E-6	-9.15E-9	0.45±0.06	37.85^{x}±1.65	0.59±0.22	0.84^{y} ±0.03	1555.93^{y}±99.21
	P	1	5.93^{y}±0.22	0.069±0.01	-0.0011±0.0001	5.36 E-6	-9.13E-9	0.58±0.03	41.76^{xy}±0.76	0.60±0.19	0.85^{y}± 0.02	1501.55^{y}±46.51
		2	5.22^{y}±0.26	0.079±0.009	-0.0010±0.0001	4.65E-6	-7.52E-9	0.51±0.03	40.03^{xy}±0.91	0.54±0.21	0.89^{x}± 0.02	1565.45^{y}±55.03
	S × P	1	5.46^{y}±0.17	0.089±0.006	-0.0012±0.0001	5.39E-6	-8.48E-9	0.64±0.02	41.80^{xy}±0.61	0.67±0.08	0.88^{xy} ±0.01	1537.39^{y}±37.36
		2	6.08^{x}±0.18	0.071±0.007	-0.0009±0.0001	4.41E-6	-7.03E-9	0.58±0.02	39.92^{xy}±0.65	0.67±0.09	0.84^{y}± 0.01	1656.85^{xy}±39.37
Effects of breeds × years	A × P	1999	6.57^{x}±0.55	0.164^{x}±0.02	-0.0026±0.0003	0.00001^{y}±1.55E-6	-2.19E-8	0.69^{x}±0.0.07	46.23^{y}±1.96	0.71±0.26	0.90^{x}±0.04	1858.15^{x}±118.40
		2000	6.00^{xy}±0.37	0.083^{xy}±0.01	-0.0012±0.0002	5.33E-6	-8.5E-9	0.52^{xy}±0.05	39.66^{x}±1.30	0.55±0.17	0.91^{x}±0.03	1693.92^{y}±78.31
	H × P	1999	6.13^{x}±0.30	0.081^{xy}±0.01	-0.0011±0.0001	5.16E-6	-8.45E-9	0.53^{xy}±0.04	42.42^{xy}±1.05	0.61±0.14	0.83^{y}±0.02	1720.99^{xy}±63.29
		2000	5.78^{y}±0.16	0.099^{xy}±0.006	-0.0013±0.0001	5.70E-6	-8.98E-9	0.59^{xy}±0.02	41.01^{xy}±0.57	0.64±0.07	0.88^{xy} ±0.01	1766.24^{xy}±34.69
		2001	6.62^{x}±0.44	0.074^{y}±0.02	-0.0009±0.0002	4.04E-6±1.24E-6	-6.23E-9	0.53^{xy}±0.06	42.88^{xy}±1.56	0.58±0.21	0.84^{y}±0.03	1861.33^{x}±94.45
	J × P	1999	6.05^{xy}±0.93	0.092^{xy}±0.03	-0.0011±0.001	3.75E-6±2.59E-6	-4.2E-9	0.48^{y}±0.12	42.10^{xy}±3.28	0.50±0.43	0.84^{y}±0.07	1795.76^{x}±198.11
		2000	5.38^{y}±0.45	0.072^{y}±0.02	-0.0009±0.0002	4.43E-6±1.26E-6	-7.29E-9	0.47^{y}±0.05	38.35^{x} ±1.60	0.64±0.13	0.86^{xy} ±0.03	1470.97^{y}±96.67
	P	1999	6.12^{x}±0.28	0.069^{y}±0.01	-0.0012±0.0001	6.26E-6	-1.11E-9	0.59^{xy}±0.04	42.10^{xy}±0.98	0.59±0.13	0.86^{xy} ±0.03	1456.49^{y}±60.28
		2000	5.32^{y}±0.21	0.076^{y}±0.008	-0.001±0.00011	4.51E-6	-7.27E-9	0.54^{xy}±0.03	40.24^{x}±0.74	0.68±0.10	0.85^{y}±0.02	1567.25^{y}±45.45
		2001	6.13^{x}±0.78	0.060^{y}±0.03	-0.0008±0.0004	3.28E-6±2.19E-6	-4.43E-9	0.43^{y}±0.10	44.16^{xy}±2.77	0.63±0.37	0.88^{xy} ±0.02	1550.85^{y}±167.44
	S × P	1999	5.39^{y}±0.21	0.095^{xy}±0.007	-0.0013±0.0001	6.14E-6	-1.01E-8	0.64^{x}±0.03	42.03^{xy}±0.73	0.66±0.10	0.87^{xy}± 0.01	1514.04^{y}±44.52
		2000	6.08^{xy}±0.16	0.068^{y}±0.006	-0.0009±0.0001	3.95E-6	-6E-9	0.59^{xy}±0.02	40.26^{x}±0.58	0.68±0.07	0.86^{y}±0.01	1634.30^{y}±35.02
		2001	4.02^{y}±0.69	0.157^{x}±0.02	-0.0019^{x}±0.00034	9.02E-6±1.93E-6	-1.47E-8	0.71^{x}±0.09	40.40^{x}±2.32	0.63±0.31	0.87^{xy}± 0.05	1757.18^{xy}±147.67

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination; RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at P < 5%.

Table A 2.4: Least square means (±SE) of different parameters (a, b, c, d and k), fit statistics and predicted milk yield for the Sikka model

Effects			Model parameters			Fit statistics				Predicted milk yield
			a	b	c	R^2	AIC	RootMSPE	CCC	
Effects of years	1999		7.44±0.20	0.0009^{y}±0.0004	-0.00002 ±3.64E-6	0.74 ± 0.017	20.84 ±1.20	0.88 ±0.48	0.79± 0.015	2000.08 ±57.43
	2000		6.90±0.15	0.0024^{xy}±0.0003	-0.00002 ±2.74E-6	0.74 ±0.013	22.50±0.90	0.91± 0.42	0.79 ±0.012	1954.42 ±43.22
	2001		6.78±0.42	0.0049^{x}±0.0009	-0.00005±7.738E-6	0.66 ±0.037	22.24±2.55	0.94 ±0.70	0.78 ± 0.03	2004.64 ±122.07
Effects of season	1		7.09 ± 0.17	0.0021±0.0005	-0.00002±3.098E-6	0.76 ±0.021	20.98 ±1.01	0.93 ±0.44	0.80 ±0.019	1896.17^{y} ±69.25
	2		7.02 ±0.16	0.0027±0.0004	-0.00002±2.999E-6	0.73 ±0.016	22.96±0.98	0.88 ±0.44	0.78±0.014	2012.57^{x} ±51.98
Effects of seasons × breeds	A × P	1	8.41^{x}±0.48	-0.00006^{y}±0.001	-8.96E-6±9.054E-6	0.72^{y}± 0.042	19.12^{x} ±2.95	0.80^{xy} ±0.75	0.83^{x} ±0.038	2258.63^{x} ±140.98
		2	8.31^{x}±0.55	0.0017^{xy}±0.0012	-0.00002 ±0.00001	0.68^{y} ±0.048	25.34^{y} ±3.36	0.76^{xy} ±0.81	0.69^{y} ±0.042	2470.00^{x} ±160.74
	H × P	1	7.52^{xy}±0.24	0.0023^{x}±0.0005	-0.00003 ±4.422E-6	0.73^{y}± 0.021	24.19^{y} ±1.44	0.85^{xy} ±0.53	0.79^{xy} ± 0.019	2144.09^{x}±68.85
		2	7.16^{xy}±0.22	0.0036^{x}±0.0004	-0.00002 ±4.129E-6	0.76^{xy}± 0.019	22.98^{xy} ±1.35	0.74^{xy} ±0.51	0.81^{x} ±0.018	2095.48^{x} ±64.29
	J × P	1	5.16^{y}±1.00	0.007^{xy}±0.0021	-0.00004 ±0.00002	0.91^{x}± 0.088	23.02^{xy}±6.14	0.65^{x} ±1.09	0.77^{xy} ±0.078	1450.91^{y}±293.47
		2	6.15^{xy}±0.55	0.0029^{x}±0.0012	-0.00002 ±0.00001	0.72^{y} ±0.048	19.96^{x} ±3.36	0.85^{xy}± 0.81	0.78^{xy}±0.043	1774.22^{y} ±160.74
	P	1	6.98^{xy}±0.26	-0.00077^{y}±0.0005	-9.22E-6 ±4.787E-6	0.75^{xy} ±0.02	20.25^{x}±1.56	1.23^{y}± 0.55	0.82^{x}±0.019	1809.38^{xy} ±74.54
		2	6.03^{xy}±0.30	0.0028^{x}±0.0004	-0.00002 ±5.64E-6	0.71^{y}± 0.026	25.58^{y} ±1.84	1.13^{y}±0.60	0.82^{x}±0.023	1708.35^{y}±87.82
	S × P	1	6.79^{xy}±0.21	0.0022^{x}±0.0004	-0.00002±3.847E-6	0.72^{y}± 0.018	20.44^{x} ±1.25	0.84^{xy}± 0.49	0.79^{xy}±0.016	1817.85^{xy} ±59.90
		2	7.39^{xy}±0.22	0.0023^{x}±0.0004	-0.00002 ±4.08E-6	0.77^{xy} ±0.019	22.86^{xy} ±1.33	0.88^{xy} ±0.51	0.78^{xy} ±0.017	2014.81^{xy}±63.54
Effects of breeds × years	A × P	1999	10.19^{x}±0.66	-0.001^{y}±0.0014	-0.00001±0.000012	0.72^{xy} ±0.058	20.88^{xy}±4.04	0.77^{xy} ±0.88	0.80 ±0.052	2711.97^{x}±192.18
		2000	7.56^{xy}±0.43	0.0014^{xy} ±0.0009	-0.00001±8.047E-6	0.69^{y} ±0.038	22.24^{xy}±2.67	0.79^{xy} ±0.72	0.76 ±0.034	2192.41^{x} ±127.12
	H × P	1999	7.56^{xy}±0.35	0.0013^{xy} ±0.0007	-0.00002±6.503E-6	0.75^{xy}± 0.031	20.63^{xy}±2.16	0.70^{x} ±0.65	0.81 ±0.028	2133.44^{xy} ±102.73
		2000	7.28^{xy}±0.19	0.0029^{x} ±0.0004	-0.00002 ±3.566E-6	0.75^{xy}± 0.017	23.96^{xy} ±1.18	0.82^{xy} ±0.48	0.81± 0.015	2100.29^{xy} ±56.32
		2001	7.17^{xy}±0.52	0.0068^{x}±0.0011	-0.00007 ±9.705E-6	0.71^{xy} ±0.046	26.91^{y} ±3.22	0.75^{x}± 0.79	0.78 ±0.041	2216.15^{x}±153.31
	J × P	1999	7.62^{xy}±1.09	0.0017^{xy}±0.0023	-0.00002 ±0.00002	0.93^{x}±0.096	15.74^{x} ±6.76	0.73^{x} ±1.14	0.79 ±0.086	2108.93^{xy} ±321.58
		2000	5.51^{y}±0.54	0.0044^{x} ±0.0011	-0.00002±9.934E-6	0.72^{xy}± 0.047	21.83^{xy}±3.30	0.83^{xy}± 0.80	0.78 ±0.042	1602.15^{y} ±156.92
	P	1999	7.28^{xy}±0.33	-0.0014^{y} ±0.00069	-8.79E-6±6.083E-6	0.77^{xy} ±0.029	22.16^{xy}±2.02	1.21^{y} ±0.62	0.83 ±0.026	1846.17^{xy} ±96.09
		2000	6.23^{y}±0.25	0.0019^{xy} ±0.00053	-0.00002±4.622E-6	0.72^{xy} ±0.022	22.97^{xy} ±1.53	1.20^{y}±0.50	0.81 ±0.019	1740.65^{xy} ±73.01
		2001	5.79^{y}±0.93	0.0016^{xy} ±0.0019	-0.00001±0.000017	0.56^{y}±0.082	18.3^{x}±5.71	0.81^{xy} ±1.05	0.82 ± 0.073	1500.49^{y} ±271.79
	S × P	1999	7.06^{xy}±0.25	0.0021^{x} ±0.0005	-0.00002 ±4.552E-6	0.71^{xy} ±0.022	21.07^{xy} ±1.51	0.85^{xy}± 0.54	0.77 ±0.019	1851.76^{xy} ±71.91
		2000	7.09^{xy}±0.19	0.0023^{x} ±0.0004	-0.00002 ±3.577E-6	0.76^{xy} ±0.017	22.12^{xy}±1.19	0.83^{xy} ±0.48	0.80± 0.015	1940.39^{xy} ±56.49
		2001	6.97^{xy}±0.78	0.0037^{x} ±0.0017	-0.00002 ±0.000014	0.67^{y} ±0.068	17.94^{x}±4.78	1.32^{y} ±0.93	0.80 ±0.061	2014.56^{xy} ±227.39

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination; RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at P < 5%.

Table A 2.5: Least square means (±SE) of different parameters (a, b, c, d and k), fit statistics and predicted milk yield for the Ali Polynomials

ffects			Model parameters					Fit statistics				Predicted milk yield
			a	b	c	d	k	R2	AIC	RootMSPE	CCC	
Effects of years	1999		-11.57^{y} ±5.03	21.87^{x} ± 7.42	14.12^{x}±3.10	-6.30 ± 2.49	-2.83±0.52	0.92 ± 0.009	11.49 ±0.43	0.55 ± 0.02	0.016± 0.01	989.01^{y}±93.58
	2000		0.71^{xy}± 3.79	6.89^{y} ±5.59	5.69^{y} ±2.33	-3.43± 1.87	-1.32±0.39	0.88 ± 0.007	11.59± 0.32	0.56 ±0.017	0.015 ±0.008	1061.57^{x}±70.43
	2001		6.67^{x} ±10.69	0.062^{y} ±15.77	1.75^{y} ±6.59	-2.08 ±5.29	-0.60±1.11	0.91 ± 0.019	10.10 ±0.91	0.51 ±0.05	0.012 ±0.024	1067.83^{x}±198.89
Effects of seasons	1		-5.65^{y} ±4.23	4.87^{y}± 7.93	9.95±2.61	-1.82^{x}±2.66	-2.06±0.44	0.91 ±0.009	11.79± 0.46	0.58 ± 0.019	0.015 ±0.009	1038.66±78.46
	2		0.23^{x} ±4.11	12.66^{x} ±6.67	6.14 ±2.54	-5.16^{y} ±2.23	-1.41 ±0.43	0.88 ±0.008	11.37 ±0.39	0.54 ±0.018	0.015 ±0.009	1043.38±76.28
Breed Group	A × P		-13.89^{y} ±9.97	26.12^{x} ±14.70	16.51^{x}±6.14	-7.27 ±4.93	-3.29 ±1.04	0.93 ±0.018	10.31 ±0.85	0.56 ±0.042	-0.006 ±0.02	1303.66^{x} ±185.42
	H × P		6.75^{x}±4.94	-1.14^{y}±7.28	2.56^{y} ±3.04	-1.02 ±2.44	-0.85 ±0.51	0.92 ±0.009	11.54± 0.42	0.56± 0.019	0.019± 0.009	1112.63^{xy}±91.81
	J × P		12.18^{x}±12.93	-10.25^{y} ±19.07	-2.09^{y} ±7.97	2.21 ±6.39	-0.032 ±1.34	0.85 ±0.023	11.27 ±1.10	0.57 ±0.06	0.023± 0.027	1152.38^{xy}±240.50
	P		-9.51^{y}±5.86	21.05^{x} ±8.64	11.36^{x} ±3.61	-7.92 ±2.89	-2.18 ±0.61	0.89 ±0.011	11.50± 0.49	0.56 ±0.02	0.023 ±0.01	769.14^{y}±108.91
	S × P		-2.43^{y} ±4.94	11.94^{xy}±7.29	7.62^{xy} ±3.05	-5.68± 2.44	-1.62 ±0.51	0.91±0.009	10.68± 0.42	0.54 ±0.017	0.014 ±0.008	859.54^{y}±91.91
Effects of seasons × breeds	A × P	1	-5.91^{y} ±13.38	13.37^{xy} ±19.71	10.97 ±8.25	-2.67^{y} ± 6.60	-2.31 ±1.39	0.90±0.02	10.19± 1.15	0.61 ±0.06	-0.003±0.03	1307.43^{x}±250.92
		2	-24.51^{y} ±12.81	41.35^{x}±18.87	23.64 ±7.90	-12.19^{y} ±6.32	-4.56± 1.33	0.93±0.02	11.38± 1.10	0.51 ±0.06	-0.008 ±0.03	1300.24^{x}±240.24
	H × P	1	-6.09^{y} ±5.63	17.18^{xy}± 8.30	10.29 ±3.48	-6.73^{y}± 2.78	-2.12 ±0.59	0.90 ±0.01	11.90± 0.49	0.57± 0.03	0.032 ±0.02	1112.01^{xy}±105.69
		2	21.43^{x} ±5.98	-22.21^{y}±8.81	-6.37 ±3.69	5.48^{x} ±2.95	0.62 ±0.62	0.92±0.01	11.92± 0.52	0.54 ±0.03	0.0059 ±0.01	1129.29^{xy}±112.21
	J × P	1	35.48^{x} ±20.92	-46.36^{y}±30.81	-14.89 ±12.91	14.76^{x} ±10.32	2.10 ±2.18	0.92±0.04	13.44 ±1.80	0.61 ±0.09	0.036 ±0.05	1304.58^{xy}±392.31
		2	-0.55^{y}± 15.22	9.15^{xy}±22.42	4.89 ±9.39	-4.51^{y} ±7.51	-1.10 ±1.58	0.78±0.03	10.89 ±1.31	0.55 ±0.07	0.018 ±0.03	1084.26^{xy}±285.45
	P	1	-19.82^{y} ±6.89	34.48^{x}±10.15	18.12 ±4.25	-11.31^{y} ±3.39	-3.35 ±0.72	0.91±0.01	12.09 ±0.59	0.58 ±0.03	0.019 ±0.02	703.00^{y}±129.18
		2	-2.41^{y}± 7.15	11.20^{xy}±10.53	6.75 ±4.41	-5.18^{y} ± 3.53	-1.41 ±0.74	0.86 ±0.01	11.75 ±0.62	0.55 ±0.03	0.028 ±0.016	834.15^{y}±134.12
	S × P	1	1.05^{xy} ±5.30	5.67^{xy}±7.81	5.76 ±3.27	-3.16^{y} ±2.62	-1.35 ±0.55	0.91± 0.009	11.32± 0.46	0.56 ±0.02	0.0034 ±0.01	883.77^{y}±99.47
		2	10.64^{x}± 5.46	23.79^{x} ±8.05	12.59 ± 3.37	-9.38^{y}± 2.69	-2.44 ±0.57	0.89 ±0.01	10.90 ±0.47	0.52 ±0.02	0.025 ±0.01	824.89^{y}±102.44
Effects of breeds × years	A × P	1999	1.35^{x}±16.66	-1.63^{y}±24.58	9.28^{xy} ± 10.26	4.99^{x} ±8.25	-2.29± 1.73	0.94 ±0.03	12.29^{y} ±1.44	0.78^{y}±0.08	-0.017 ±0.04	1451.39^{x} ± 313.73
		2000	-23.04^{y}± 11.02	40.92^{x}±16.26	21.21^{x} ±6.79	-13.17^{y} ±5.46	-4.00 ±1.14	0.90± 0.02	10.16^{xy} ±0.95	0.46^{x} ±0.05	-0.001 ±0.025	1239.06^{x} ±207.51
	H × P	1999	-13.04^{y} ±8.90	26.76^{x}±13.14	14.66^{x} ±5.49	-9.85^{y} ± 4.41	-2.83 ± 0.92	0.93±0.02	11.54^{xy}± 0.77	0.54^{xy} ±0.04	0.034± 0.02	893.42^{xy}±167.42
		2000	8.84^{xy}±4.88	-4.53^{y}± 7.20	1.40^{y}±3.00	0.28^{xy} ± 2.42	-0.69± 0.51	0.90 ±0.009	12.14^{y}±0.42	0.57^{xy} ±0.02	0.015± 0.01	1174.04^{xy}±91.95
		2001	36.33^{x}± 13.29	-40.23^{y} ±19.61	-16.86^{y} ± 8.19	9.37^{x}± 6.58	2.63±1.38	0.93±0.02	11.07^{xy} ±1.15	0.54^{xy} ±0.06	0.024 ±0.03	1225.65^{x}±250.27
	J × P	1999	53.73^{x}±27.87	-73.36^{y} ±41.13	-26.13^{y} ±17.17	24.37^{x} ± 13.81	3.96± 2.89	0.89± 0.05	11.60^{xy}± 2.41	0.58^{xy} ±0.13	0.024 ±0.06	1473.68^{x}±524.97
		2000	1.97^{xy} ±13.59	5.01^{xy} ±20.07	3.79^{xy}± 8.38	-3.13^{y} ± 6.74	-0.93 ±1.41	0.82± 0.03	11.82^{xy} ±1.17	0.56^{xy}± 0.06	0.024 ±0.03	1085.97^{y}±256.16
	P	1999	-38.22^{y}± 8.33	59.12^{x} ±12.29	30.05^{x}±5.13	-17.83^{y} ± 4.13	-5.42 ±0.86	0.92±0.02	12.61^{y}±0.72	0.56^{xy} ±0.04	0.009 ±0.019	544.09^{y}±156.87
		2000	4.48^{xy} ±6.33	1.87^{y} ±9.34	2.36^{y}± 3.89	-2.61^{y} ± 3.13	-0.65± 0.66	0.86 ±0.01	11.9^{y}±0.55	0.58^{xy} ±0.03	0.027 ±0.014	908.86^{xy}±119.19
		2001	-17.90^{y}±23.56	33.08^{x} ±34.76	15.89^{x}±14.51	-12.22^{y} ± 11.67	-2.91 ±2.44	0.89 ±0.04	6.81^{x} ±2.03	0.38^{x} ±0.11	0.071± 0.05	564.35^{y}±443.68
	S × P	1999	-3.65^{y} ±6.23	11.19^{xy} ±9.19	8.97^{xy} ±3.84	-3.92^{y} ± 3.09	-1.96 ±0.65	0.93±0.01	10.73^{xy} ±0.54	0.50^{xy} ±0.03	0.018 ±0.01	943.21^{xy}±117.39
		2000	-3.65^{y} ±4.89	14.14^{xy} ±7.23	8.10^{xy} ±3.02	-6.82^{y} ± 2.43	-1.64 ± 0.51	0.89 ±0.009	11.34^{xy}± 0.42	0.56^{xy} ±0.02	0.015± 0.01	800.27^{y}±92.23
		2001	-30.19^{y} ±19.71	52.55^{x} ±29.08	25.94^{x} ± 12.14	-18.28^{y}± 9.76	-4.95 ± 2.04	0.91 ±0.04	11.26^{xy} ±1.70	0.56^{xy} ±0.09	-0.042 ± 0.04	864.85^{y}±371.21

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination; RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at $P < 5\%$.

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Table A 2.6: Least square means (±SE) of different parameters (a, b, c, d and k), fit statistics and predicted milk yield for the Legendre Polynomials

Effects			Model parameters					Fit statistics				Predicted milk yield
			a	b	c	d	k	R2	AIC	RMSPE	CCC	
Effects of years	1999		5.81±0.17	0.092±0.006	-0.0003 ±0.0004	-3.43E-7±1.955E-6	1.557E-9	0.95 ±0.003	116.74±1.57	1.38±0.06	0.67±0.01	1919.86 ± 44.68
	2000		5.79±0.13	0.083±0.005	-0.0008± 0.0003	2.382E-6±1.477E-6	-2.33E-9	0.95±0.003	118.89 ± 1.18	1.35±0.05	0.66±0.009	1932.16 ± 33.76
	2001		6.05±0.35	0.089±0.013	-0.0010±0.0009	3.216E-6±4.167E-6	-3.38E-9	0.95±0.007	121.80 ± 3.34	1.43±0.13	0.68±0.03	2071.97± 95.26
Effects of season	1		5.88±0.20	0.085±0.005	-0.0009±0.0003	1.988E-6±2.375E-6	-2.61E-9	0.96±0.004	117.47 ± 1.91	1.31±0.07	0.67±0.01	1923.39 ± 37.79
	2		5.68±0.15	0.087±0.004	-0.0005±0.0003	1.135E-6±1.783E-6	-1.67E-13	0.95±0.003	119.69 ± 1.43	1.40±0.06	0.66±0.01	1942.65 ± 36.58
Effects of seasons × breeds	A × P	1	6.52^{x}±0.41	0.101±0.02	-0.001 ± 0.001	3.073E-6±4.834E-6	-3E-9	0.95±0.008	119.26 ± 3.88	1.44±0.15	0.68±0.03	2168.65^{x} ± 110.20
		2	5.72^{xy}±0.46	0.117±0.02	-0.001±0.001	3.079E-6±5.512E-6	-2.8E-9	0.96±0.01	129.28 ± 4.42	1.45±0.17	0.59±0.04	2179.84^{x} ± 125.65
	H × P	1	6.25^{x}±0.19	0.084±0.007	-0.0008±0.0005	2.212E-6±2.361E-6	-2.08E-9	0.96±0.004	117.93 ± 1.89	1.25±0.07	0.64±0.02	2097.87^{x}± 53.82
		2	5.68^{xy}±0.19	0.098±0.007	0.0003±0.0005	-3.17E-6±2.205E-6	5.424E-9	0.95±0.004	118.44 ± 1.77	1.38±0.07	0.69±0.01	2007.25^{x} ± 50.26
	J × P	1	5.27^{y}±0.85	0.060±0.031	-0.0004±0.002	3.268E-7±0.00001	3.33E-10	0.95±0.02	119.53 ± 8.08	1.45±0.31	0.69±0.07	1646.34^{y} ± 229.40
		2	5.58^{xy}±0.46	0.080±0.02	-0.0007±0.0011	2.137E-6±5.512E-6	-2.15E-9	0.94±0.01	119.29 ± 4.43	1.57±0.17	0.64±0.04	1855.33^{xy} ± 125.65
	P	1	5.91^{xy}±0.22	0.070±0.008	-0.0007±0.0005	2.202E-6±2.556E-6	-2.13E-9	0.96±0.004	115.13 ± 2.05	1.27±0.08	0.69±0.02	1822.36^{xy} ± 58.27
		2	5.28^{y}±0.25	0.079±0.009	-0.0006±0.0006	1.858E-6±3.012E-6	-1.73E-9	0.95±0.005	114.66 ± 2.42	1.34±0.09	0.68±0.02	1761.22^{xy} ± 68.65
	S × P	1	5.48^{xy}±0.17	0.088±0.006	-0.0008±0.0004	2.125E-6±2.054E-6	-1.92E-9	0.97±0.004	115.51 ± 1.65	1.13±0.06	0.68±0.01	1770.93^{xy} ± 46.83
		2	6.13^{x}±0.18	0.071±0.007	-0.0007±0.0005	1.766E-6±2.179E-6	-1.55E-9	0.96±0.004	116.80 ±1.75	1.24±0.07	0.66±0.01	1919.24^{xy} ± 49.67
Effects of breeds × years	A × P	1999	6.57^{x}±0.56	0.164±0.02	-0.0017±0.0014	5.235E-6±6.56E-6	-5.21E-9	0.97±0.01	116.38 ± 5.26	1.27±0.20	0.64±0.04	2457.89^{x} ± 149.80
		2000	6.00^{xy}±0.37	0.083±0.01	-0.0008±0.0009	2.131E-6±4.339E-6	-1.91E-9	0.95 ±0.007	126.78 ± 3.48	1.53±0.13	0.65±0.03	2049.10^{xy} ± 99.08
	H × P	1999	6.08^{xy}±0.29	0.074± 0.01	0.0021±0.0007	-0.00001±3.471E-6	1.636E-8	0.94±0.006	116.64 ± 2.78	1.55±0.11	0.66±0.02	2005.65^{xy} ± 79.27
		2000	5.81^{xy}±0.16	0.099±0.006	-0.0008±0.0004	2.29E-6±1.928E-6	-2.07E-9	0.96±0.003	117.15 ± 1.55	1.24±0.06	0.66±0.01	2036.37^{xy} ± 44.04
		2001	6.62^{x}±0.44	0.074±0.016	-0.0006±0.0011	1.617E-6±5.233E-6	-1.41E-9	0.96 ±0.009	129.46 ± 4.19	1.35±0.16	0.69±0.04	2245.41^{x}± 119.50
	J × P	1999	6.05^{xy}±0.93	0.092±0.033	-0.0007±0.0023	1.5E-6±0.000011	-8E-10	0.94 ±0.02	125.00 ± 8.79	1.93±0.34	0.61±0.07	2035.74^{x} ± 250.66
		2000	5.38^{xy}±0.45	0.072±0.02	-0.0006±0.0011	1.772E-6±5.356E-6	-1.76E-9	0.94±0.009	118.00 ± 4.29	1.46±0.17	0.67±0.04	1752.67^{xy}± 122.31
	P	1999	6.04^{xy}±0.28	0.073±0.009	-0.0008±0.0007	2.508E-6±3.251E-6	-2.47E-9	0.96±0.006	115.66 ± 2.61	1.24±0.10	0.72±0.02	1843.92^{xy} ± 74.24
		2000	5.37^{xy}±0.21	0.076±0.008	-0.0007±0.0005	1.845E-6±2.505E-6	-1.74E-9	0.95±0.004	114.49 ± 2.01	1.29±0.08	0.67±0.02	1768.49^{xy} ± 57.21
		2001	6.13^{x}±0.79	0.061±0.03	-0.0005±0.002	1.31E-6±9.277E-6	-8.57E-12	0.93 ±0.02	115.14 ± 7.44	1.83±0.29	0.76±0.06	1800.37^{xy}± 211.85
	S × P	1999	5.40^{xy}±0.21	0.094±0.008	-0.0009±0.0005	2.431E-6±2.455E-6	-2.32E-9	0.96±0.004	113.39 ± 1.97	1.14±0.08	0.67±0.02	1750.47^{y} ± 56.05
		2000	6.08^{xy}±0.16	0.067±0.006	-0.0006±0.0004	1.571E-6±1.928E-6	-1.3E-9	0.96 ±0.003	118.10 ± 1.55	1.22±0.06	0.68±0.01	1891.08^{xy} ± 44.04
		2001	4.88^{y}±0.66	0.140±0.02	-0.0012±0.0016	3.455E-6±7.762E-6	-3.2E-9	0.98±0.01	111.35 ± 6.22	1.02±0.24	0.65±0.05	1627.41^{y}± 177.24

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination;
RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at P < 5%.

Table A 2.7: Least square means (±SE) of different parameters (a, b, c, d and k), fit statistics and predicted milk yield for the Nelder model

Effects			Model parameters				Fit statistics				Predicted milk yield
			a	b	c	d	R^2	AIC	RootMSPE	CCC	
Effects of years	1999		0.079^{y} ±0.03	1.08 ± 0.32	0.0008 ±0.0007	-1.46E-6 ±4.299E-6	0.75 ±0.01	68.34±0.92	0.032^{xy}±0.002	0.90 ±0.01	1861.44 ±56.61
	2000		0.056^{xy} ±0.023	1.43 ±0.24	0.0017 ±0.0005	-8.21E-6 ±3.232E-6	0.73 ±0.01	65.58 ±0.51	0.033^{y}± 0.002	0.89 ±0.01	1835.77 ±42.56
	2001		0.032^{x} ±0.065	1.59 ±0.67	0.0022 ± 0.002	-0.00001 ±9.138E-6	0.78 ±0.03	67.29± 1.37	0.027^{x}±0.004	0.90 ±0.03	1904.48 ±120.32
Effects of seasons	1		0.061 ± 0.026	1.55^{x} ±0.38	0.0015 ±0.0006	-8.72E-6^{y} ±5.163E-6	0.74 ± 0.02	66.06 ±0.54	0.039^{y}± 0.002	0.89 ±0.02	1773.91 ±68.12
	2		0.062 ±0.025	0.99^{y} ±0.29	0.0015 ± 0.0006	-1.55E-6^{x} ±3.876E-6	0.74 ±0.01	66.44± 0.52	0.031^{x}±0.002	0.91 ±0.01	1880.68± 51.13
Effects of seasons × breeds	A × P	1	-0.293^{x} ±0.075	4.69^{x} ±0.77	0.0097^{x} ±0.002	-0.00006 ± 0.00001	0.74^{xy} ±0.03	67.80 ±1.58	0.029 ±0.005	0.86 ±0.03	2109.54^{x} ±138.67
		2	0.065^{xy} ± 0.09	1.02^{y} ±0.88	0.0004^{xy} ±0.002	2.461E-7 ± 0.00001	0.80^{x} ± 0.04	70.69 ±1.80	0.026 ±0.006	0.92 ±0.04	2233.88^{x}± 158.11
	H × P	1	0.117^{y} ±0.04	0.49^{y} ± 0.38	-0.00004^{y} ±0.0008	2.778E-6 ± 5.134E-6	0.78^{xy} ±0.02	68.03 ±0.77	0.034±0.002	0.89 ± 0.02	2030.23^{xy} ±67.73
		2	0.029^{xy} ±0.03	1.73^{xy} ± 0.35	0.0018^{x} ±0.0007	-9.25E-6 ±4.794E-6	0.79^{x} ±0.02	69.53 ±0.72	0.025 ±0.002	0.89 ±0.01	1924.28^{xy} ±63.24
	J × P	1	0.203^{y} ± 0.16	0.74^{y} ±1.61	-0.0015^{y} ± 0.0036	0.00001 ±0.00002	0.71^{xy} ±0.07	62.73 ±3.29	0.063 ±0.01	0.92 ±0.07	1317.91^{y} ±288.67
		2	0.159^{y} ±0.09	0.74^{y} ±0.88	-0.00018^{y} ± 0.002	2.403E-6 ±0.00001	0.66^{y} ± 0.04	61.17 ±1.80	0.034 ± 0.006	0.94 ±0.04	1695.45^{xy} ±158.11
	P	1	0.096^{xy} ± 0.039	0.80^{y} ±0.41	0.0007^{xy} ±0.0009	6.061E-7 ±5.558E-6	0.74^{xy} ±0.02	65.73 ±0.84	0.046 ±0.003	0.86 ±0.02	1717.14^{xy} ±73.32
		2	0.163^{y} ±0.047	0.37^{y} ±0.48	-0.0003^{y} ±0.001	3.213E-6 ±6.548E-6	0.71^{xy} ± 0.02	64.18 ±0.99	0.037 ±0.003	0.91 ± 0.02	1623.93^{y} ±86.39
	S × P	1	0.091^{xy} ±0.032	1.02^{y} ±0.33	0.0006^{xy} ±0.0007	-9.01E-7 ±4.467E-6	0.74^{xy} ± 0.01	66.68 ±0.67	0.04±0.002	0.90 ± 0.01	1694.75^{xy} ±58.92
		2	0.073^{xy} ±0.034	1.10^{y} ± 0.35	0.001^{xy} ±0.0007	-4.36E-6 ±4.738E-6	0.74^{xy} ±0.01	66.91 ±0.71	0.031 ±0.002	0.89 ±0.01	1925.89^{xy} ±62.49
Effects of breeds × years	A × P	1999	0.067^{xy} ± 0.11	0.63^{y} ± 1.09	0.0005 ±0.002	6.852E-7 ±0.00002	0.82^{x} ±0.05	71.33^{y}± 2.23	0.029 ±0.007	0.78^{y} ±0.04	2563.66^{x} ±196.39
		2000	-0.217^{x} ±0.07	4.07^{x} ±0.69	0.008 ± 0.008	-0.00004 ±9.358E-6	0.75^{xy} ±0.03	68.16^{xy} ±1.40	0.027 ±0.004	0.92^{x}± 0.03	2006.00^{xy} ±123.26
	H × P	1999	0.106^{y} ±0.05	0.72^{y} ±0.56	0.0002 ± 0.001	1.878E-6 ± 7.602E-6	0.77^{xy} ±0.02	68.21^{xy}± 1.14	0.038± 0.004	0.93^{x} ±0.02	1980.35^{xy} ±100.14
		2000	0.049^{xy} ± 0.03	1.41^{xy} ±0.31	0.0014 ± 0.007	-6.72E-6 ±4.224E-6	0.78^{xy} ±0.01	68.90^{xy}± 0.63	0.027 ±0.002	0.88^{xy} ± 0.01	1947.59^{xy} ±55.63
		2001	0.144^{y} ± 0.08	0.22^{y} ±0.84	-0.0007 ± 0.002	6.456E-6 ± 0.00001	0.83^{x} ±0.04	69.73^{y} ±1.72	0.022± 0.006	0.91^{x} ±0.03	2150.16^{x} ±150.96
	J × P	1999	0.109^{y} ± 0.17	0.66^{y} ±1.77	0.00003 ±0.004	1.915E-6 ± 0.00002	0.73^{xy} ±0.08	69.34^{y} ±3.60	0.038± 0.012	0.92^{x}± 0.07	1956.47^{xy}±316.66
		2000	0.184^{y} ± 0.08	0.76^{y} ±0.86	-0.0006 ±0.002	4.702E-6 ±0.00001	0.66^{y} ±0.04	59.67^{x}± 1.76	0.041± 0.006	0.94^{x} ±0.04	1525.43^{y}± 154.52
	P	1999	0.075^{xy} ±0.05	0.95^{y} ±0.52	0.0009 ± 0.001	3.121E-7 ± 7.12E-6	0.75^{xy} ±0.02	65.76^{xy} ±1.07	0.049 ±0.003	0.89^{xy} ± 0.02	1735.13^{y}± 93.79
		2000	0.15^{y} ±0.04	0.43^{y} ±0.40	-0.0009 ±0.0009	2.475E-6 ±5.487E-6	0.71^{xy} ±0.02	64.74^{x} ±0.82	0.038 ±0.003	0.87^{xy} ± 0.02	1661.81^{y}±72.27
		2001	0.15^{y} ±0.15	0.55^{y} ± 1.49	0.00008 ±0.003	2.331E-6 ± 0.00002	0.74^{xy} ±0.06	64.20^{x} ±3.04	0.037 ±0.01	0.94^{x} ±0.06	1437.18^{y} ±267.63
	S × P	1999	0.106^{y} ± 0.04	0.86^{y} ±0.39	0.00015 ±0.0009	1.967E-6 ±5.349E-6	0.75^{xy} ±0.02	67.08^{xy}± 0.80	0.042 ±0.003	0.90^{x} ±0.02	1730.72^{y} ±70.46
		2000	0.086^{xy} ±0.03	0.99^{y} ± 0.31	0.0008 ±0.0007	-2.9E-6 ± 4.237E-6	0.73^{xy} ±0.01	66.45^{xy} ±0.63	0.033 ±0.002	0.91^{x} ± 0.01	1849.10^{xy}± 55.80
		2001	-0.212^{x} ±0.12	4.13^{x} ±1.25	0.0073 ±0.003	-0.00004 ±0.00002	0.78^{xy} ±0.05	69.29^{y} ±2.55	0.026± 0.008	0.85^{xy} ±0.05	1804.95^{xy} ±223.91

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination; RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at $P < 5\%$.

Table A 2.8: Least square means (±SE) of different parameters (a, b, c, d and k), fit statistics and predicted milk yield for the Wilmink model

Effects			Model parameters			Fit statistics				Predicted milk yield
			a	b	c	R^2	AIC	RootMSPE	CCC	
Effects of years	1999		9.03 ±0.22	-0.021^{y} ±0.001	-4.53 ±0.32	0.79 ±0.01	26.26 ±0.61	0.35^{y} ±0.04	0.86 ±0.12	1878.29 ±57.19
	2000		8.98 ± 0.16	-0.019^{xy} ±0.001	-4.30 ±0.24	0.77 ± 0.01	25.62 ±0.46	0.33^{y} ±0.03	0.87 ±0.09	1834.90 ±43.04
	2001		9.23 ±0.46	-0.017^{x} ±0.002	-4.84 ±0.69	0.77 ±0.03	23.03 ±1.29	0.51^{x} ±0.09	0.87 ±0.26	1888.67 ±121.55
Effects of seasons	1		8.69^{y}± 0.18	-0.019 ±0.001	-3.45 ±0.27	0.79 ± 0.02	26.43 ±0.73	0.38 ±0.05	0.85 ±0.15	1829.44 ±48.15
	2		9.28^{x} ±0.18	-0.019 ± 0.001	-4.69 ±0.26	0.77 ± 0.01	25.60 ± 0.55	0.33 ±0.04	0.89 ±0.11	1866.91 ±46.62
Effects of seasons × breeds	A × P	1	9.33^{xy} ±0.53	-0.018 ±0.002	-2.46 ±0.78	0.73^{y} ± 0.04	23.73 ±1.49	0.38^{xy} ±0.11	0.84^{y} ± 0.30	2138.92^{x} ±140.12
		2	10.73^{x} ±0.61	-0.025 ±0.002	-5.29 ±0.89	0.72^{y} ±0.04	26.11 ±1.70	0.28^{x} ±0.12	0.87^{xy} ± 0.34	2257.59^{x} ±159.76
	H × P	1	9.51^{xy} ±0.26	-0.020 ±0.001	-4.11 ± 0.38	0.79^{xy} ±0.02	25.55 ±0.73	0.38^{xy} ± 0.05	0.86^{xy} ±0.15	2027.99^{x} ±68.43
		2	10.15^{x} ±0.24	-0.021 ±0.001	-6.24 ±0.36	0.82^{xy} ±0.02	26.12 ± 0.68	0.32^{xy} ±0.05	0.86^{xy} ±0.14	1917.21^{xy} ±63.90
	J × P	1	8.27^{xy} ±1.10	-0.022 ± 0.004	-6.28 ±1.62	0.87^{x} ±0.08	29.32 ± 3.11	0.38^{xy} ±0.23	0.83^{y} ±0.62	1310.34^{y} ±291.67
		2	8.10^{xy} ±0.61	-0.015 ±0.002	-3.94 ± 0.89	0.76^{xy} ±0.04	23.64 ±1.70	0.19^{x} ±0.12	0.98^{x} ±0.34	1685.39^{xy} ±159.76
	P	1	7.74^{y} ±0.28	-0.018 ±0.001	-1.86 ± 0.41	0.80^{xy} ±0.02	27.47 ±0.79	0.44^{y} ±0.06	0.87^{xy} ±0.16	1736.73^{xy} ±74.09
		2	8.32^{xy} ±0.33	-0.017 ± 0.001	-4.38 ± 0.48	0.76^{xy} ±0.02	25.64 ±0.93	0.44^{y} ±0.07	0.87^{xy} ±0.19	1609.81^{y} ±87.28
	S × P	1	8.88^{xy} ±0.23	-0.021 ±0.001	-4.29 ±0.33	0.78^{xy} ± 0.02	26.09 ±0.63	0.34^{xy} ±0.05	0.86^{xy} ±0.13	1699.07^{xy} ±59.54
		2	9.34^{xy} ± 0.24	-0.020 ±0.001	-4.01 ± 0.35	0.80^{xy} ± 0.02	26.51 ± 0.67	0.41y ±0.05	0.86^{xy} ± 0.14	1921.84^{xy} ± 63.15
Effects of breeds × years	A × P	1999	11.18^{x} ± 0.73	-0.028 ± 0.003	-2.99 ± 1.08	0.73^{y} ±0.05	27.68 ±2.03	0.40^{x} ±0.15	0.83^{y} ± 0.41	2528.94^{x} ± 191.26
		2000	9.39^{xy} ± 0.48	-0.018 ±0.002	-3.99 ± 0.71	0.72^{y} ±0.03	23.49 ±1.35	0.31^{x} ± 0.09	0.86^{xy} ±0.27	2042.45^{xy} ±126.50
	H × P	1999	9.51^{xy} ± 0.39	-0.022 ±0.002	-4.05 ±0.58	0.81^{xy} ±0.03	26.71 ± 1.09	0.43^{x} ± 0.08	0.86^{xy} ±0.22	2018.71^{xy} ±102.23
		2000	9.93^{xy} ±0.21	-0.021 ±0.001	-5.59 ±0.32	0.79^{xy} ±0.01	25.93 ±0.59	0.29^{x} ±0.04	0.86^{xy} ±0.12	1934.02^{xy} ±56.05
		2001	10.04^{x} ± 0.58	-0.017 ±0.002	-5.33 ± 0.86	0.84^{x} ±0.04	23.39 ±1.62	0.53^{xy} ±0.12	0.82^{y} ±0.33	2115.48^{x} ± 152.57
	J × P	1999	9.62^{xy} ± 1.21	-0.021 ± 0.005	-4.41 ±1.80	0.89^{x} ±0.08	26.02 ±3.40	0.23^{x} ±0.25	0.93^{x} ±0.69	1968.88^{x} ± 320.03
		2000	7.79^{y} ±0.59	-0.015 ±0.002	-4.50 ±0.88	0.75^{xy} ± 0.04	24.69 ± 1.66	0.24^{x} ±0.12	0.85^{xy} ±0.34	1510.73^{y} ±156.16
	P	1999	7.85^{y} ±0.36	-0.019 ±0.001	-1.59 ± 0.54	0.82^{x} ±0.02	27.69 ± 1.02	0.42^{x} ±0.07	0.87^{xy} ±0.21	1768.05^{xy} ±95.63
		2000	8.11^{xy} ±0.28	-0.016 ±0.001	-3.67 ± 0.41	0.78^{xy} ±0.02	26.20 ± 0.77	0.42^{x} ±0.06	0.86^{xy} ±0.16	1652.72^{y} ±72.66
		2001	7.26^{y} ±1.03	-0.016 ±0.004	-3.01 ± 1.52	0.65^{y} ±0.07	25.79 ±2.88	0.79^{y} ±0.21	0.90^{x} ±0.58	1535.47^{y} ±270.48
	S × P	1999	9.14^{xy} ±0.27	-0.022 ±0.001	-4.36 ± 0.40	0.78^{xy} ±0.02	26.12 ±0.76	0.34^{x} ±0.06	0.85^{xy} ±0.15	1726.52^{xy} ±71.56
		2000	9.01^{xy} ±0.21	-0.019 ±0.001	-3.88 ±0.32	0.79^{xy} ±0.01	26.65 ±0.60	0.39^{x} ±0.04	0.87^{xy} ±0.12	1851.71^{xy} ±56.22
		2001	10.02^{xy} ±0.86	-0.022 ±0.003	-6.69 ±1.27	0.79^{xy} ±0.06	22.28 ±2.41	0.31^{x} ± 0.17	0.84^{xy} ±0.49	1803.31^{xy} ±26.30

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination; RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at P < 5%.

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Table A 2.9: Least square means (±SE) of different parameters (a, b, c, d and k), fit statistics and predicted milk yield for the Rook model

Effects			Model parameters				Fit Statistics				Predicted milk
			a	b	c	d	R^2	AIC	RootMSPE	CCC	yield
Effects of years	1999		34.39 ± 95.53	426.70±10921	50806±21698	0.0035±0.0003	0.62±0.02	23.03±0.67	1.32±0.55	0.67±0.02	1927.84±59.87
	2000		162.03 ± 71.89	1495.26^{x}±8219.01	59563±16330	0.0026±0.0002	0.65±0.02	22.37±0.50	1.40±0.41	0.69±0.01	1997.16±45.06
	2001		26.99± 203.04	-4616.50^{y}±23211	55825±46118	0.0021±0.001	0.68±0.04	18.77±1.42	0.75±1.17	0.65±0.05	2032.92±127.24
Effects of seasons	1		42.33^{y} ±72.66	412.46±9193.85	51126±18265	0.0030±0.00025	0.66±0.01	22.68±0.56	1.23±0.46	0.69 ± 0.02	1921.00^{y}±50.35
	2		191.98^{x} ±80.37	1487.99±8901.23	62188±17683	0.0026±0.00024	0.63±0.02	22.21±0.55	1.46±0.45	0.68 ± 0.02	2037.39^{x}± 48.74
Breed group	A × P		7.89^{y} ±12.22	2121.12±39164	56248±46017	0.0026±0.0003	0.56±0.04	20.58 ±1.32	0.94±1.01	0.60±0.04	2299.66^{x}±118.62
	H × P		21.34^{x}	-6856.98±19006	-2537.35±22332	0.0028±0.0002	0.66±0.02	21.33 ± 0.66	1.47±0.45	0.67±0.02	2183.54^{x}±58.74
	J × P		12.38^{xy}±6.96	-10054±22319	248382±61291	0.0021±0.00018	0.69±0.05	20.83 ±1.71	1.15±1.36	0.75±0.05	1820.12^{y}±153.86
	P		5.54^{y} ±16.28	-3301.42±42164	-10033±22364	0.0026±0.0004	0.65±0.02	22.85±0.77	1.43±0.55	0.71±0.02	1819.25^{y}±69.67
	S × P		20.52^{x}±5.94	-21409±19034	-7707±22364	0.0025±0.00015	0.66±0.02	21.37±0.66	1.65±0.42	0.68±0.02	1973.96^{xy}±58.80
Effects of seasons × breeds	A × P	1	8.00 ± 234.56	-250.64 ±26908	371.43±53218	0.0028±0.001	0.60±0.05	22.06±1.65	0.70±1.35	0.62±0.06	1960.54^{xy}±146.02
		2	52.68 ±267.44	216.14±30680	-269.14±60678	0.0027±0.001	0.52±0.06	21.38±1.88	1.15±1.54	0.56±0.07	2641.05^{x}±166.49
	H × P	1	21.73 ±114.56	164.62±13142	2082.72±25992	0.0030±0.0003	0.69±0.02	21.92±0.81	1.45±0.66	0.66±0.03	2202.88^{x}±71.32
		2	180.52± 106.98	-1556.55 ±12272	31.45±24271	0.0028±0.003	0.64±0.02	22.28±0.75	1.51±0.62	0.68±0.03	2121.94^{x}±66.60
	J × P	1	736.77 ±488.28	6771.89±56013	206.64±110782	0.0026±0.002	0.72±0.10	26.83±3.44	0.67±2.82	0.83±0.12	1395.00^{y}±303.96
		2	9.71± 267.44	-284.79±30680	373179±60678	0.0018±0.001	0.67±0.06	20.47±1.89	1.37±1.54	0.73±0.07	1901.53^{xy}±166.49
	P	1	47.26 ±124.02	-10245±14227	-366.72±28139	0.0039±0.0003	0.65±0.03	24.37±0.87	1.18±0.72	0.72±0.03	1788.60^{xy}±77.21
		2	520.03± 146.12	16637±16762	-17.16±33152	0.0027±0.0004	0.66±0.03	23.28±1.03	1.68±0.85	0.70±0.04	1765.15^{xy}±90.96
	S × P	1	32.46± 99.67	8369.10±11434	-5997.28±22613	0.0029±0.0003	0.67±0.02	22.64±0.70	1.57±0.57	0.69±0.03	1815.73^{xy}±62.05
		2	65.80 ±105.72	-2327.90±12127	-209.64±23985	0.0028±0.0004	0.65±0.02	22.25±0.75	1.71±0.61	0.68±0.03	2061.36^{x}±65.81
Effects of breeds × years	A × P	1999	10.83 ± 321.60	1.36±36707	-7.32±72764	0.0036±0.001	0.56±0.07	26.63^{y}±2.23	0.71±1.85	0.65^{xy}±0.08	2508.90^{x} ±200.15
		2000	34.69 ±212.72	-69.16±24280	136.78±48129	0.0023±0.001	0.57±0.05	19.64^{x}±1.48	0.99±1.22	0.57^{y}±0.05	2145.95^{x}± 132.39
	H × P	1999	13.66 ± 171.90	-5630.88±19621	-445.50±38894	0.0042±0.001	0.64±0.04	22.57^{xy}±1.19	1.57±0.98	0.65^{xy}±0.04	2055.75^{xy}±106.99
		2000	147.38 ± 94.25	942.35±10758	1788.33±21325	0.0027±0.0003	0.67±0.02	22.35^{xy}±0.65	2.53±0.54	0.68^{xy}±0.02	2152.92^{x}±58.66
		2001	10.96 ± 256.55	-2468.86±29282	-1760.06±58045	0.0017±0.001	0.67±0.05	19.30^{x}±1.78	0.75±1.47	0.61^{y}±0.06	2440.86^{x}± 159.67
	J × P	1999	7.67 ± 538.15	-21.72±611423	-34.81±121757	0.0018±0.002	0.66±0.11	22.60^{xy}±3.74	0.63±3.09	0.91^{x}±0.13	2215.16^{x}±334.92
		2000	217.92± 262.59	1668.77±29971	355476±59411	0.0020±0.001	0.68±0.06	21.78^{xy}±1.82	1.32±1.51	0.71^{xy}±0.07	1682.14^{y}±163.42
	P	1999	70.18 ± 160.80	-18242±18354	-403.41±36382	0.0047±0.0005	0.63±0.03	25.24^{y}±1.11	1.38±0.92	0.68^{xy}±0.04	1786.49^{xy}±100.08
		2000	357.06 ± 122.18	13562±13945	19.57±27644	0.0026±0.0003	0.66±0.03	23.81^{y}±0.85	1.47±0.70	0.73^{xy}±0.03	1792.23^{xy}±76.04
		2001	96.08 ± 454.82	-18864±51912	-2080.17±102904	0.0038±0.002	0.69±0.09	14.74^{x}±3.14	0.72±2.61	0.80^{x}±0.11	1530.70^{y}±283.06
	S × P	1999	22.81± 120.33	15598±13735	-1020.47±27226	0.0029±0.0004	0.62±0.03	22.17^{xy}±0.84	1.60±0.69	0.66^{xy}±0.03	1800.99^{xy}±74.89
		2000	66.13 ± 94.54	-4029.17±10791	-4861.64±21391	0.0029±0.0003	0.68±0.02	22.71^{xy}±0.66	1.67±0.55	0.70^{xy}±0.02	2004.27^{xy}±58.84
		2001	10.23± 380.53	6.16±43433	-81.03±86095	0.0027±0.0012	0.77±0.08	21.29^{xy}±2.64	1.58±2.19	0.61^{y}±0.09	2052.93^{xy}±236.82

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination; RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at $P < 5\%$.

Table A 2.10: Least square means (±SE) of different parameters (a, b, c, d and k), fit statistics and predicted milk yield for the Dijkstra model

Effects			Model parameters				Fit statistics				Predicted milk yield
			a	b	c	d	R^2	AIC	RootMSPE	CCC	
Effects of years	1999		4.94±0.27	0.094^{xy}±0.01	0.088±0.053	0.03±0.0079	0.16±0.015	24.74±0.64	5.07±1.77	0.017±0.007	1732.29±52.69
	2000		4.83 ±0.21	0.11^{x}±0.0107	0.092±0.039	0.031±0.0059	0.18±0.011	23.41±0.48	4.73±1.54	0.025±0.005	1756.91±39.65
	2001		5.43 ±0.58	0.056^{y}±0.03	0.16±0.11	0.027±0.017	0.17±0.03	21.34±1.37	5.11±2.59	0.074±0.015	1857.25±111.98
Effects of seasons	1		4.87 ±0.23	0.085±0.012	0.10±0.045	0.024±0.0067	0.19±0.029	24.12±0.54	5.12±1.63	0.023±0.005	1711.95±44.31
	2		4.89 ±0.22	0.11±0.012	0.086±0.043	0.037±0.0065	0.17±0.015	23.35±0.53	4.68±1.60	0.025±0.006	1790.83±42.90
Breed group	A × P		5.16±0.54	0.095±0.028	0.0904±0.10	0.0059±0.016	0.12±0.038	22.52±1.27	5.07±2.49	0.046±0.014	2053.79^{x}±104.40
	H × P		5.31 ±0.27	0.098±0.014	0.12±0.052	0.032±0.0078	0.19±0.017	23.97±0.63	4.93±1.76	0.032±0.007	1941.90^{xy}±51.69
	J × P		4.41 ± 0.70	0.078±0.037	0.056±0.14	0.046±0.02	0.18±0.015	23.34±1.65	4.53±2.84	0.059±0.018	1548.87^{y}±135.41
	P		5.44±0.32	0.068±0.017	0.18±0.062	0.037±0.009	0.19±0.017	23.26±0.75	5.22±1.92	0.028±0.008	1623.72^{xy}±61.32
	S × P		5.02±0.27	0.087±0.014	0.12±0.052	0.025±0.0078	0.18±0.015	22.72±0.63	5.06±1.76	0.028±0.007	1742.48^{xy}±51.75
Effects of seasons × breeds	A × P	1	5.24±0.67	0.098 ±0.035	0.058±0.13	0.0032±0.019	0.24±0.037	23.99±1.59	4.88±2.79	0.036±0.017	1926.03^{xy}±129.23
		2	4.59 ±0.77	0.13±0.039	0.082±0.15	0.013±0.022	0.12±0.042	22.09±1.81	5.02±2.98	0.022±0.019	2144.60^{x}±147.35
	H × P	1	5.50±0.33	0.099±0.017	0.17±0.064	0.035±0.0095	0.19±0.017	24.35±0.78	5.07±1.95	0.022±0.008	1965.84^{xy}±63.12
		2	4.84 ±0.31	0.12±0.016	0.045±0.059	0.032±0.0089	0.16±0.017	24.25±0.72	4.55±1.88	0.019±0.007	1881.77^{xy}±58.94
	J × P	1	3.08 ±1.40	0.089±0.073	0.035±0.27	0.039±0.041	0.056±0.077	28.57±3.31	4.51±4.04	0.009±0.035	1301.00^{y}±269.02
		2	4.53 ±0.77	0.098±0.039	0.034±0.15	0.049±0.022	0.14±0.042	22.43±1.81	4.29±2.98	0.054±0.019	1584.26^{y}±147.35
	P	1	5.18±0.36	0.057±0.018	0.17 ±0.069	0.019±0.011	0.19±0.019	24.19±0.84	5.16±2.03	0.009±0.008	1577.32^{y}±68.33
		2	5.40 ±0.42	0.12±0.022	0.14±0.081	0.065±0.012	0.20±0.022	23.45±0.99	5.07±2.20	0.018±0.011	1617.75^{y}±80.50
	S × P	1	4.61±0.29	0.092±0.015	0.062±0.055	0.022±0.0083	0.17±0.016	23.77 ± 0.67	5.15±1.82	0.013±0.007	1615.98^{y}±54.91
		2	5.12±0.30	0.11±0.016	0.15±0.059	0.0304±0.0088	0.20±0.017	22.94±0.72	4.75±1.87	0.014±0.007	1819.76^{xy}±58.24
Effects of breeds × years	A × P	1999	4.00 ± 0.92	0.17±0.048	0.10±0.18	0.0062±0.027	0.20±0.05	28.07±2.15	5.43±3.26	0.045±0.022	2048.81^{x}±176.68
		2000	5.37 ± 0.61	0.087±0.031	0.055±0.12	0.0078±0.018	0.18±0.03	21.02±1.42	4.72±2.65	0.023±0.015	2008.92^{x}±116.86
	H × P	1999	5.49 ± 0.49	0.13±0.025	0.057±0.094	0.064±0.014	0.18±0.03	26.10±1.15	4.94±2.38	0.018±0.012	1933.84^{xy}±94.44
		2000	4.89 ± 0.27	0.12±0.014	0.13±0.052	0.027±0.0078	0.17±0.015	23.98±0.63	4.71±1.76	0.016±0.007	1890.29^{xy}±51.78
		2001	6.33 ± 0.73	0.032±0.038	0.015±0.14	0.019±0.021	0.21±0.04	22.61 ± 1.71	5.15±2.91	0.062±0.018	2119.21^{x}±140.94
	J × P	1999	5.25 ± 1.54	0.049±0.079	0.044±0.29	0.0041±0.045	0.059±0.084	23.86±3.59	2.80±4.82	0.06±0.038	1962.00^{xy}±295.64
		2000	3.94± 0.75	0.11±0.039	0.032±0.14	0.058±0.022	0.14±0.04	23.84±1.75	4.63±2.94	0.039±0.019	1413.40^{y}±144.26
	P	1999	5.60± 0.46	0.044±0.024	0.23±0.088	0.021±0.013	0.18±0.03	25.74±1.07	5.16±2.30	-0.0026±0.01	1598.16^{y}±88.34
		2000	5.08 ± 0.35	0.11±0.018	0.063±0.067	0.047±0.01	0.21±0.019	23.34±0.82	5.14±2.03	0.017±0.009	1601.62^{y}±67.12
		2001	5.24 ± 1.30	0.082±0.067	0.87±0.25	0.053±0.038	0.049±0.07	16.46±3.04	4.69±3.87	0.093±0.032	1460.79^{y}±249.87
	S × P	1999	4.69 ± 0.34	0.095±0.018	0.066±0.066	0.022±0.0099	0.17±0.018	23.01±0.80	5.31±1.97	0.004±0.009	1629.09^{y}±66.94
		2000	4.99 ± 0.27	0.11±0.014	0.13±0.052	0.028±0.0078	0.19±0.015	23.61±0.63	4.71±1.77	0.016±0.007	1760.04^{xy}±51.94
		2001	4.32 ± 1.09	0.11±0.056	0.045±0.21	0.035±0.032	0.21±0.059	23.38±2.54	5.47±3.55	0.053±0.027	1759.33^{xy}±209.05

Legends: A = Australian-Friesian-Sahiwal; H = Holstein; S= Sahiwal; P = Pabna; J = Jersey; AIC = Akaike Information criteria; R^2 = Coefficient of determination; RootMSPE = Root mean square prediction error; CCC= Concordance correlation coefficients. a, b, c, d and k are the model parameters that define the scale and shape of the curve.

Means with different superscripts are different at P < 5%.

APPENDIX TWO (B)

Figures of lactation curves for different genotypes by fitting 10 different lactation curves

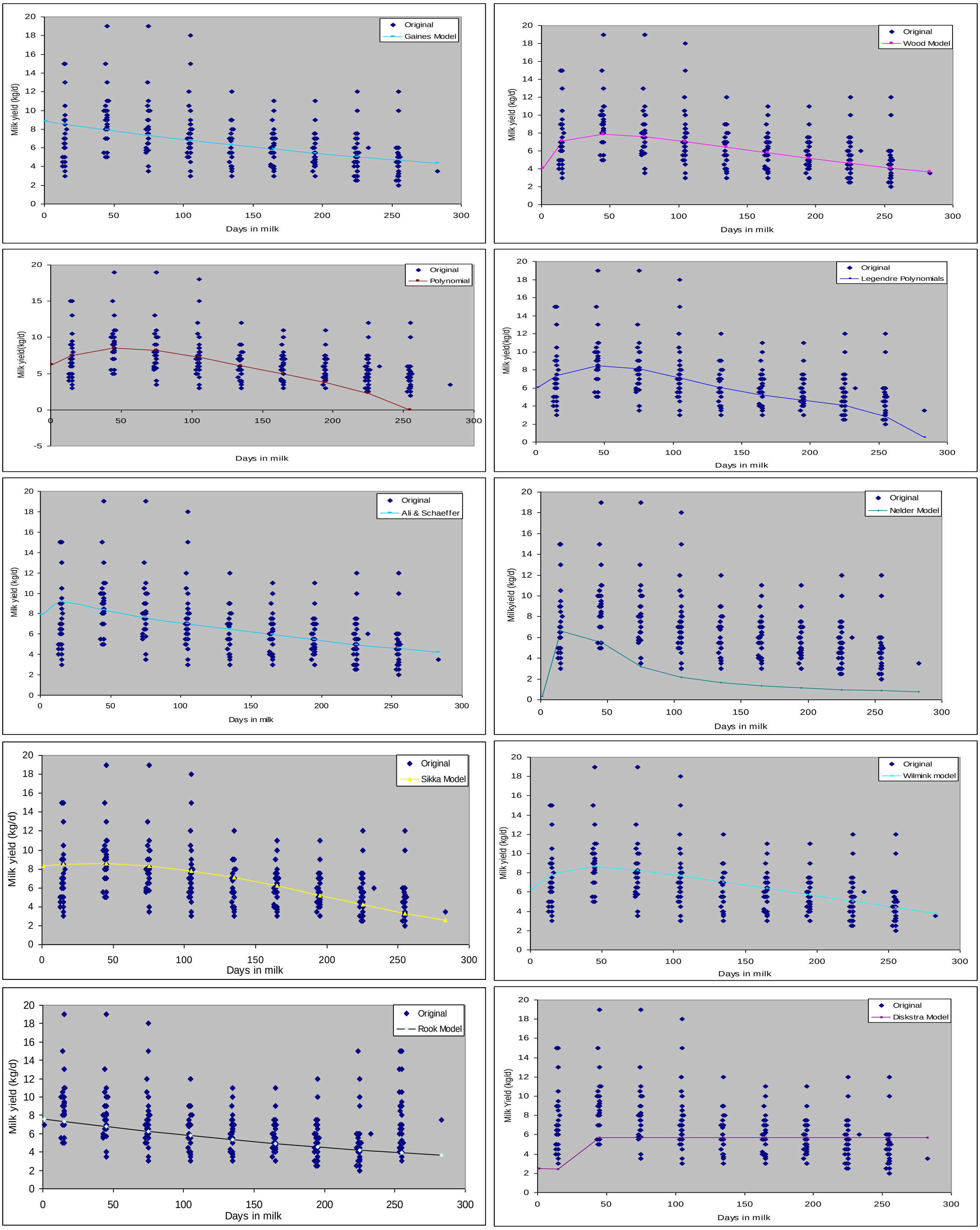

Figure 4.3: Lactation curves for Australian-Friesian-Sahiwal × Pabna cows. Lines were obtained by fitting the candidate functions: Gaines, Wood, Polynomials, Legendre Polynomials, Ali and Schaeffer polynomial regression, Nelder, Sikka, Wilmink, Rook and Dijkstra equations

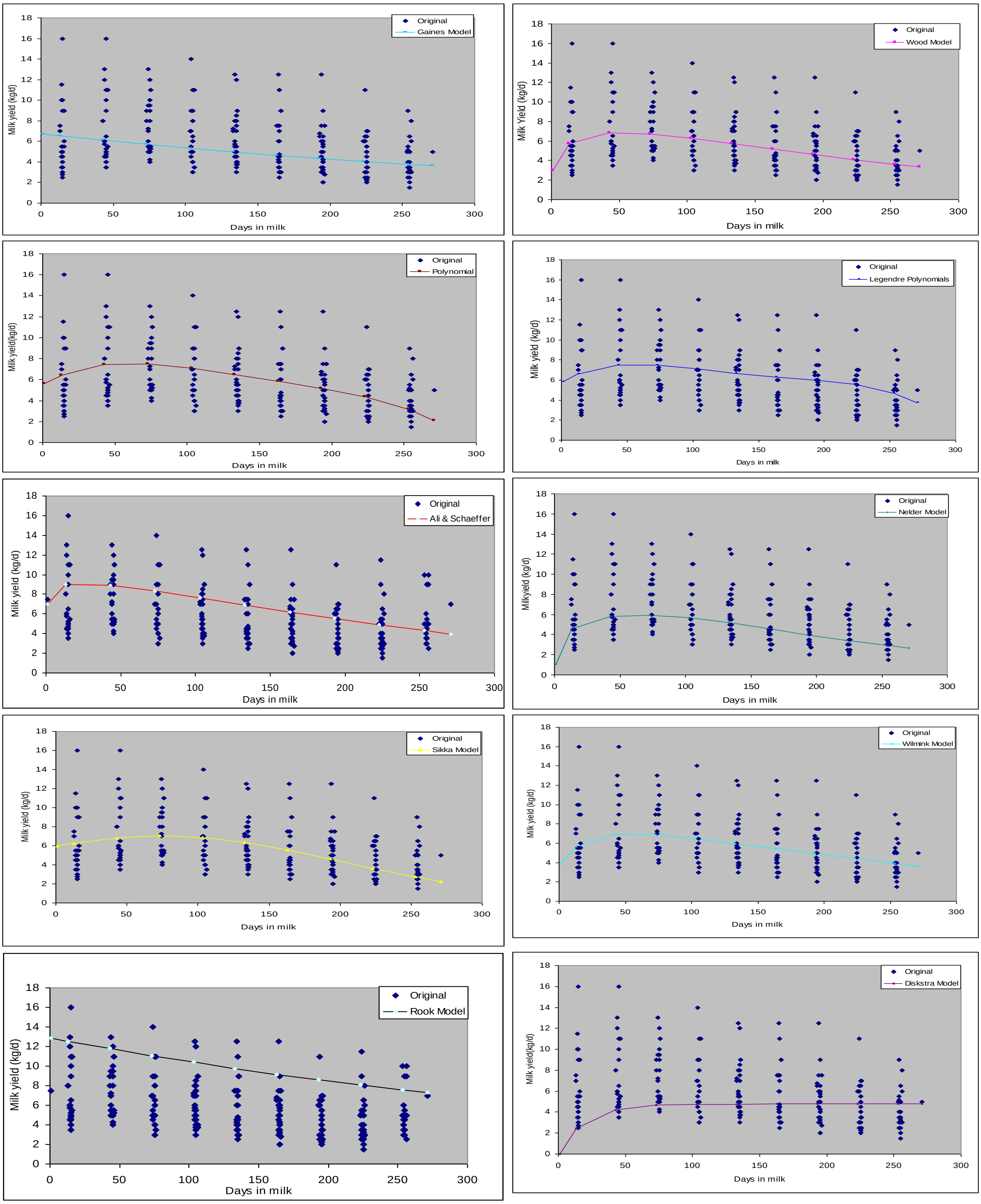

Figure 4.4: Lactation curves for Jersey × Pabna cows. Lines were obtained by fitting the candidate functions: Gaines, Wood, Polynomial, Legendre Polynomials, Ali and Schaeffer polynomial regression, Nelder, Sikka, Wilmink, Rook and Dijkstra equations

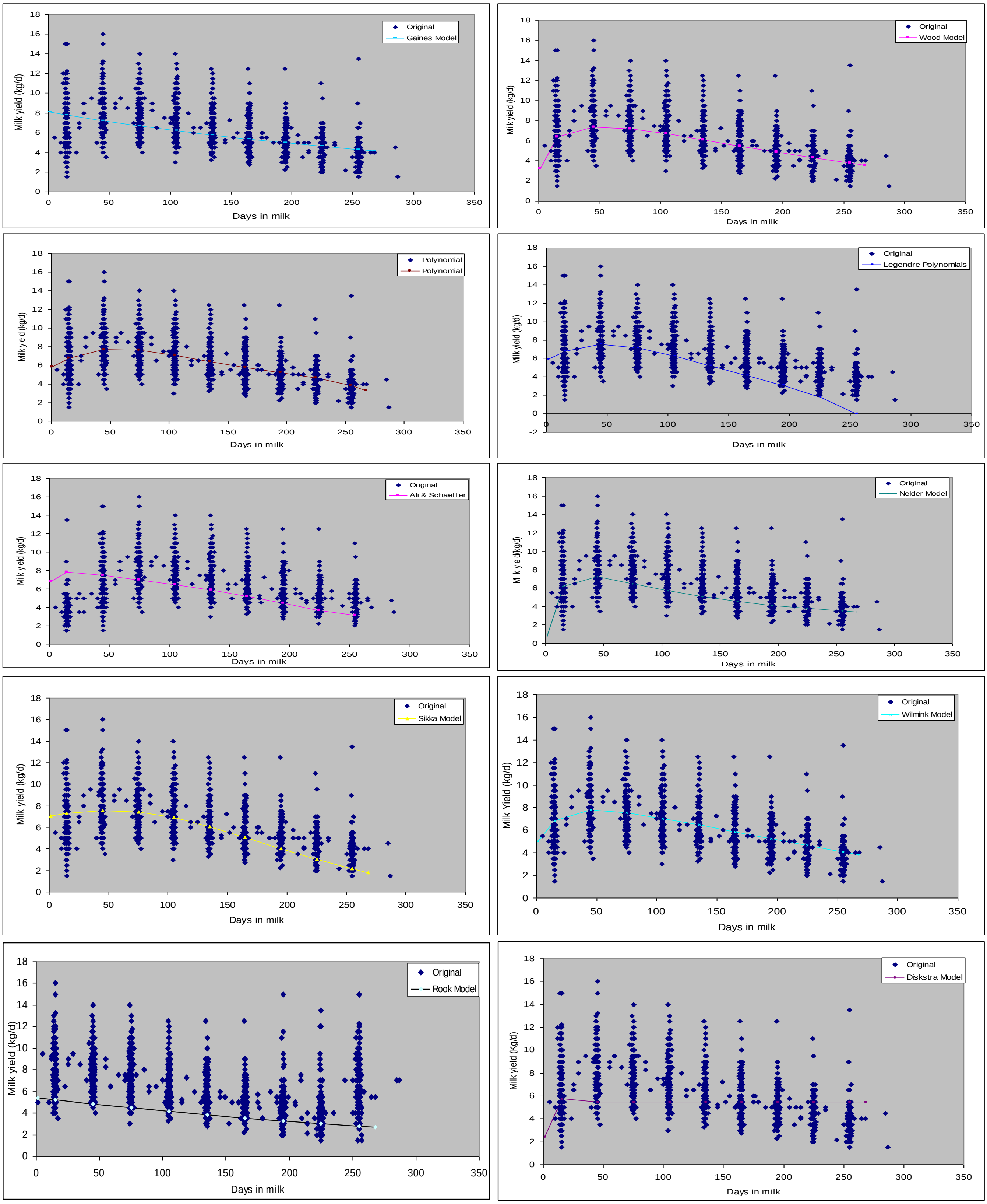

Figure 4.5: Lactation curves for Sahiwal × Pabna cows. Lines were obtained by fitting the candidate functions: Gaines, Wood, Polynomial, Legendre Polynomials, Ali and Schaeffer polynomial regression, Nelder, Sikka, Wilmink, Rook and Dijkstra equations

APPENDIX THREE (A)

SAS CODE FOR MULTITRAIT STOCHASTIC SIMULATION MODEL

/*Multitrait simulation for base year*/

```
proc iml;
nh = 200; /*number of herd*/
/*herd size: 45 to 60*/
hs=J(nh,1,0); do k=1 to nh; hs[k]=round(15*Uniform(0)+45); end;
/*means and covariance matrices*/
MeanM= 1782.29; MeanF= 77.7; MeanP= 71.4; MeanL= 259.4; MeanLg= 2752;
SireID=0; DamID=0;

sigma0={689.06  42.13  37.72  15.67   30.54,
         42.13   6.49   4.90   7.83   14.82,
        37.72   4.90   5.93   7.27    2.20,
        15.67   7.83   7.27  21.08    1.18,
        30.54  14.82   2.20   1.18  167.18};/*Herd effects*/
          r1={0, 0, 0, 0, 0 };
        h1=(root(sigma0)); /*Cholesky decomposition*/

sigma1={17915.62   360.75   267.83   222.13    193.49,
          360.75    22.35    16.86    32.36     65.62,
          267.83    16.86    18.92    26.62      5.03,
          222.13    32.36    26.62   107.58     20.99,
          193.49    65.62     5.03    20.99    835.92};/*Breeding values*/
          mu={0, 0, 0, 0, 0};
          g=(root(sigma1));

sigma2={34453.13    754.64 539.33 205.75  2552.92,
           754.64    38.92  29.63  40.24    89.85,
           539.33    29.63  37.09  39.64    51.05,
           205.75    40.24  39.64  88.76    15.72,
          2552.92    89.85  51.05  15.72 15548.20};/*Temporary
                                           environmental effects*/
          mu1={0, 0, 0, 0, 0};
        g1=(root(sigma2));

sigma3={16537.5   388.86   272.18  128.94  259.37,
          388.86   21.53    16.05   27.07   34.31,
          272.18   16.05    19.67   26.11    5.45,
          128.94   27.07    26.11   72.61    2.08,
          259.37   34.31     5.45    2.08  334.36};/*Permanent
                                             environmental effects */
          mu2={0, 0, 0, 0, 0};
          g2=(root(sigma3));

nh60=nh*60; /*define maximum number of cows*/
/*define datasets for storage*/
MeanHerd=J(nh60,6,0); MHname={MY FY PY Lwt Longe CowID};
HerdEffect=J(nh60,6,0); HEname={HMY HFY HPY HLwt HLonge CowID};
BreedEffect=J(nh60,6,0); BEname={BMY BFY BPY BLwt BLonge CowID};
EnvTEffect=J(nh60,6,0); ETname={ETMY ETFY ETPY ETLwt ETLonge CowID};
EnvPEffect=J(nh60,6,0); EPname={EPMY EPFY EPPY EPLwt EPLonge CowID};
AgeEffect=J(nh60,6,0); AEname={AMY AFY APY ALwt ALonge CowID};
MeanAll=J(nh60,6,0); MAname={MMY MFY MPY MLwt MLonge CowID};
HerdCow=J(nh60,6,0); HCname={CowID Herd Cow Age SireID DamID};

nh60k=0; /*start: count total number of animals*/
do i = 1 to nh;
   hs1=hs[i]; /*herd size: 45 to 60*/
   h2=normal(repeat(r1`,1,1));
   k10=h2*h1;
   k11=repeat(k10,hs1); /*Herd effects*/
   b1=Normal(repeat(mu`,hs1,1));
   a1=b1*g; /*Breeding values*/
   b2=Normal(repeat(mu1`,hs1,1));
   a2=b2*g1; /*Temporary environmental effects*/
   b3=Normal(repeat(mu2`,hs1,1));
   a3=b3*g2; /*Permanent environmental effects */
```

```
do j=1 to hs1;
   u1=Uniform(0);
   if u1<0.06 then do; age=10; agemy=-128;
      agefy=-6.03; agepy=-5.43; agelwt=-11.31; agel=0; end;
   if u1>=0.06 then if u1<0.13 then do; age=9; agemy=-102; agefy=-4.83;
      agepy=-4.34; agelwt=-2.49; agel=0; end;
   if u1>=0.13 then if u1<0.28 then do; age=8; agemy=-51;
      agefy=-2.41; agepy=-2.2; agelwt=-4.14; agel=0; end;
   if u1>=0.28 then if u1<0.43 then do; age=7; agemy=0;
      agefy=0; agepy=0; agelwt=0; agel=0; end;
   if u1>=0.43 then if u1<64 then do; age=6; agemy=0; agefy=0;
      agepy=0; agelwt=0; agel=0; end;
   if u1>=0.64 then if u1<0.85 then do; age=5; agemy=-64; agefy=-3.2;
      agepy=-2.72; agelwt=-18.69; agel=0; end;
   if u1>=0.85 then do; age=4; agemy=-256; agefy=-12.07;
      agepy=-10.86; agelwt=-30.57; agel=0; end;

nh60k=nh60k+1; /*count total number of animals*/
MeanHerd[nh60k,1] = MeanM + k11[j,1] + a1[j,1] + a2[j,1] + a3[j,1] + agemy;
MeanHerd[nh60k,2] = MeanF + k11[j,2] + a1[j,2] + a2[j,2] + a3[j,2] + agefy;
MeanHerd[nh60k,3] = MeanP + k11[j,2] + a1[j,2] + a2[j,2] + a3[j,2] + agepy;
MeanHerd[nh60k,4] = MeanL + k11[j,2] + a1[j,2] + a2[j,2] + a3[j,2] + agelwt;
MeanHerd[nh60k,5] = MeanLg + k11[j,2] + a1[j,2] + a2[j,2] + a3[j,2] + agel;
MeanHerd[nh60k,6] = nh60k;

do k=1 to 5;
   HerdEffect[nh60k,k] = k11[j,k]; BreedEffect[nh60k,k] = a1[j,k];
   EnvTEffect[nh60k,k] = a2[j,k]; EnvPEffect[nh60k,k] = a3[j,k];
end;
AgeEffect[nh60k,1] = agemy; AgeEffect[nh60k,2] = agefy; AgeEffect[nh60k,3] =
agepy;
AgeEffect[nh60k,4] = agelwt; AgeEffect[nh60k,5] = agel; AgeEffect[nh60k,6] =
nh60k;
HerdEffect[nh60k,6] = nh60k; BreedEffect[nh60k,6] = nh60k;
EnvTEffect[nh60k,6] = nh60k; EnvPEffect[nh60k,6] = nh60k;
HerdCow[nh60k,1] = nh60k; HerdCow[nh60k,2] = i; HerdCow[nh60k,3] = j;
HerdCow[nh60k,4] = age;
MeanAll[nh60k,1] = MeanM; MeanAll[nh60k,2] = MeanF; MeanAll[nh60k,3] =
MeanP;
MeanAll[nh60k,4] = MeanL; MeanAll[nh60k,5] = MeanLg; MeanAll[nh60k,6] =
nh60k;
end;
end;

create phenodata from MeanHerd [colname=MHname]; append from MeanHerd;
create herdeffdata from HerdEffect [colname=HEname]; append from HerdEffect;
create breedeffdata from BreedEffect [colname=BEname]; append from
BreedEffect;
create envteffdata from EnvTEffect [colname=ETname]; append from EnvTEffect;
create envpeffdata from EnvPEffect [colname=EPname]; append from EnvPEffect;
create ageeffdata from AgeEffect [colname=AEname]; append from AgeEffect;
create meandata from MeanAll [colname=MAname]; append from MeanAll;
create herdcowdata from HerdCow [colname=HCname]; append from HerdCow;
quit;

proc sort data=herdcowdata; by cowid; run;
proc sort data=meandata; by cowid; run;
proc sort data=herdeffdata; by cowid; run;
proc sort data=ageeffdata; by cowid; run;
proc sort data=breedeffdata; by cowid; run;
proc sort data=envteffdata; by cowid; run;
proc sort data=envpeffdata; by cowid; run;
proc sort data=phenodata; by cowid; run;

data Khan (where=(cowid>0));   /*final overall data set*/
merge herdcowdata meandata herdeffdata ageeffdata breedeffdata envteffdata
envpeffdata phenodata;
by cowid; run;
```

/*Year 1*/

```
filename out'C:\aireml\Herdk1.dat';
data sasuser.kkhan; set Khan; file out; put  CowID 14. SireID 10.
DamID 9. Herd 5. Age 4. MY 7.; run; quit;
filename out'C:\aireml\Herdk12.dat';
data sasuser.kkhan; set Khan; file out; put  CowID 14. SireID 10.
DamID 9. Herd 5. Age 4. FY 7.; run; quit;
filename out'C:\aireml\Herdk13.dat';
data sasuser.kkhan; set Khan; file out; put  CowID 14. SireID 10.
DamID 9. Herd 5. Age 4. PY 7.; run; quit;
filename out'C:\aireml\Herdk14.dat';
data sasuser.kkhan; set Khan; file out; put  CowID 14. SireID 10.
DamID 9. Herd 5. Age 4. LWT 7.; run; quit;
filename out'C:\aireml\Herdk15.dat';
data sasuser.kkhan; set Khan; file out; put  CowID 14. SireID 10.
DamID 9. Herd 5. Age 4. Longe 7.; run; quit;

Options noxwait xsync;
x C:\aireml\Yr11.bat;  x C:\aireml\Y2M.bat; run; quit;
  data one; infile 'C:\AIREML\uni01.sln'; input CowID EBVM;run;
quit;
x C:\aireml\Yr12.bat;  x C:\aireml\Y2M.bat; run; quit;
  data two; infile 'C:\AIREML\uni01.sln'; input CowID EBVF;run;
quit;
x C:\aireml\Yr13.bat;  x C:\aireml\Y2M.bat; run; quit;
  data three; infile 'C:\AIREML\uni01.sln'; input CowID EBVP;run;
quit;
x C:\aireml\Yr14.bat;  x C:\aireml\Y2L.bat; run; quit;
  data four; infile 'C:\AIREML\uni01.sln'; input CowID EBVLwt;run;
quit;
x C:\aireml\Yr15.bat;  x C:\aireml\Y2lg.bat; run; quit;
data five; infile 'C:\AIREML\uni01.sln'; input CowID EBVLonge;run;
quit;

data YkKK; merge one two three four five; by CowID; run; quit;

proc iml;
x= {0.32, 0, 0, 0, 0};/*economic values*/
use YKKK; read all var{EBVM EBVF EBVP EBVLWT EBVLonge} into k2;
k3=k2*x; cname={TMerit};
create k4 from k3 [colname=cname];append from k3; quit;

data k5; merge khan YKKK k4; run;

/* COWS FOR YEAR1*/
Proc sql;
create table Yk1 as
select distinct CowID, SireID, DamID, Herd, Age, MMY,MFY,MPY,MLwt,
MLonge, HMY, HFY, HPY, HLwt, HLonge, AMY, AFY, APY, ALwt, ALonge,
BMY, BFY, BPY, BLwt, BLonge, ETMY, ETFY, ETPY, ETLwt, ETLonge, EPMY,
EPFY, EPPY, EPLwt, EPLonge, MY, FY, PY, Lwt, Longe, EBVM, EBVF,
EBVP, EBVLWT, EBVLonge, Tmerit from k5; quit;

data Yk2; set Yk1; if SireID=0 then Year=0; If SireID=0 then Lac=1;
if Alonge=0 then Status=1; if Alonge=0 then k=.;run; quit;

proc rank data=Yk2 out=ranking descending fraction ties=high;
var EBVLonge;
ranks X; run;
proc sort data=ranking; by X; run; quit;
```

```
data top90 bottom10; set ranking; if X=<0.90 then output top90; else
output bottom10; run; quit;

data YKKK1; set top90; if alonge=0 then LOD=1; run;
data YKKK2; set bottom10; if alonge=0 then LOD=0; run;

data YKKK3; merge top90 YKKK1; run; quit;
data YKKK4; merge bottom10 YKKK2; run; quit;

proc sql; create table Year1bas as select distinct CowID, SireID,
DamID, Herd, Age, MMY,MFY,MPY,MLwt, MLonge, HMY, HFY, HPY, HLwt,
HLonge, AMY, AFY, APY, ALwt, ALonge, BMY, BFY, BPY, BLwt, BLonge,
ETMY, ETFY, ETPY, ETLwt, ETLonge, EPMY, EPFY, EPPY, EPLwt, EPLonge,
MY, FY, PY, Lwt, Longe, EBVM, EBVF, EBVP, EBVLWT, EBVLonge, Tmerit,
Year, Lac, Status from YKKK3; quit;

proc sql; create table Year1bas1 as select distinct
CowID, SireID, DamID, Herd, Age, MMY,MFY,MPY,MLwt, MLonge, HMY, HFY,
HPY, HLwt, HLonge, AMY, AFY, APY, ALwt, ALonge, BMY, BFY, BPY, BLwt,
BLonge, ETMY, ETFY, ETPY, ETLwt, ETLonge, EPMY, EPFY, EPPY, EPLwt,
EPLonge, MY, FY, PY, Lwt, Longe, EBVM, EBVF, EBVP, EBVLWT, EBVLonge,
Tmerit, Year, Lac, Status from YKKK4; quit;

data year1base; set year1bas year1bas1;run; quit;

proc sort data=top90; by Descending TMerit; run; quit;
data yk3; set top90 (OBS=150); if alonge=0 then status=2; run; quit;
data yk4; set khan1 (Obs=5); run; quit;
proc sql; create table Ykk as select BullID, (BullID+70153) from
Yk4; quit;
data Yk5; merge Yk4 Ykk; run; quit;

proc iml; use yk5; read all var{_TEMA001 BMY BFY BPY BLwt BLonge}
into yk6;
col={BullID BMY BFY BPY BLwt BLonge};
Yk7=30; Yk8=repeat(Yk6,Yk7); create Yk9 from Yk8 [colname=Col];
append from Yk8; quit;

proc iml; use Yk9; read all var {BMY BFY BPY BLwt BLonge} into Yk10;
use Yk3; read all var { BMY BFY BPY BLwt BLonge} into Yk11;
name={BMY BFY BPY BLwt BLonge}; Yk12=(Yk10+Yk11)/2;
create Yk13 from Yk12 [colname=name]; append from Yk12; quit;

/*Mendelian sampling*/
Proc iml;
n=150;
Sigma6 =    {12668.25   255.09      189.38      157.07      136.82,
               255.09    15.80       11.92       22.88       14.50,
               189.38    11.92       13.38       18.82        3.55,
               157.07    22.88       18.82       76.07       14.84,
               136.82    14.50        3.55       14.84      591.08};

      /* Covariance matrix for breeding values */
mu6={0, 0, 0, 0, 0};
cname={X11 X12 X13 X14 X15};
g6 =(root(sigma6)); /* Upper Triangular Cholesky decomposition of
Cov matrix */
z6=normal(repeat(mu6`, n, 1)); y6= z6*g6; create empdist6 from y6
[colname=cname];
append from y6; quit;
```

```
proc iml; use empdist6; read all var {X11 X12 X13 X14 X15} into
Yk14;
use Yk13; read all var {BMY BFY BPY BLwt BLonge} into Yk15;

Yk16=(Yk14+Yk15); KLL={BMY BFY BPY BLwt BLonge};
create Yk17 from Yk16 [colname=KLL]; append from Yk16; quit;

proc iml; use Yk17; read all var {BMY BFY BPY BLWT BLonge} into
Yk18;
use Yk3; read all var{BMY BFY BPY BLwt BLonge} into Yk19;
Yk20=Yk18-Yk19; use Yk3; read all var {My FY PY Lwt Longe} into
Yk21;
Yk22=Yk20+Yk21; MEE={MY FY PY LWT Longe};
create Yk23 from Yk22[colname=MEE]; append from Yk22; quit;

data Yk24; merge Yk3 Yk17 Yk23 Yk9; run; quit;

proc SQL;  create table Yk25 as select distinct MMY, (CowID+1000000)
from Yk24; quit;

data Yk26; merge Yk25 Yk24; run; quit;

proc sort data=Yk26; by k; run; quit;
proc surveyselect data=Yk26 Method=SRS Samprate=57 out=Yk27;
strata k; run; quit;

data yk28; set Yk27; N=ranuni(1); run;
proc sort data=Yk28; by N; run;
data Bull50 Cow50; set Yk28; if N=<0.50 then output Bull50; else
output Cow50; run;

/*Sire selection on year4*/
proc sql;
create table Bull51 as
select distinct  _Tema001,(_Tema001)as BulID, BullID,(BullID) as
SireID, CowID, (CowID) as DamID, BMY, BFY, BPY, BLWt, BLonge, Tmerit
from Bull50; quit;

proc Sql; create table Bull51F as select distinct BulID, SireID,
DamID, BMY, BFY, BPY, BLWt, BLonge, TMerit from Bull51; quit;

proc sql; create table cow51 as select distinct  _TEMA001,
BullID,CowID, Herd, Age, MMY,MFY,MPY,MLwt, MLonge, HMY, HFY, HPY,
HLwt, HLonge, AMY, AFY, APY, ALwt, ALonge, BMY, BFY, BPY, BLwt,
BLonge, ETMY, ETFY, ETPY, ETLwt, ETLonge,EPMY, EPFY, EPPY, EPLwt,
EPLonge, MY, FY, PY, Lwt, Longe,
Year, Lac, Status, k from Cow50; quit;

proc sort data=Top90; by Tmerit; run; quit;
data Yk29; set Top90(OBS=9225); run; quit;

proc iml; use Yk5; read all var{_TEMA001 BMY BFY BPY BLWT BLONGE}
into Yk30;
colll={BullID BMY BFY BPY BLwt BLonge};
Yk31=1845; Yk32=repeat(Yk30,Yk31); create Yk33 from Yk32
[colname=Colll]; append from Yk32; quit;

Proc IML;
use Yk29; read all var{BMY BFY BPY BLWT BLonge}into Yk34;
use Yk33; read all var{BMY BFY BPY BLWT BLonge} into Yk35;
Yk36=(Yk34+Yk35)/2; create Yk37 from Yk36; append from Yk36; quit;
```

```
/*Mendelian sampling*/
Proc IML;
n=9225;
sigma7 =    {12668.25   255.09      189.38      157.07      136.82,
                255.09    15.80       11.92       22.88       14.50,
                189.38    11.92       13.38       18.82        3.55,
                157.07    22.88       18.82       76.07       14.84,
                136.82    14.50        3.55       14.84      591.08};

                        /* Covariance matrix for breeding values */
mu7={0, 0, 0, 0, 0};
cname={X11 X12 X13 X14 X15};
g7 =(root(sigma7)); /* Upper Triangular Cholesky decomposition of
Cov matrix */
z7=normal(repeat(mu7`, n, 1)); y7= z7*g7; create empdist7 from y7
[colname=cname];
append from y7; quit;

proc iml; use empdist7; read all var {X11 X12 X13 X14 X15} into
Yk38;
use Yk37; read all var {col1 col2 col3 col4 Col5} into Yk39;
Yk40=(Yk38+Yk39); KLL={BMY BFY BPY BLWT BLonge};
create Yk41 from Yk40 [colname=KLL]; append from Yk40; quit;

proc iml;
use Yk41; read all var {BMY BFY BPY BLWT BLonge} into Yk42;
use Yk29; read all var{BMY BFY BPY BLwt BLonge} into Yk43;
Yk44=Yk42-Yk43; use Yk29; read all var {My FY PY Lwt Longe} into
Yk45;
Yk46=Yk44+Yk45; MEE={MY FY PY LWT Longe}; create Yk47 from
Yk46[colname=MEE];
append from Yk46; quit;

proc sql; create table Yk48 as select distinct  CowID, SireID,
DamID, Herd, Age, MMY,MFY,MPY,MLwt, MLonge, HMY, HFY, HPY, HLwt,
HLonge, AMY, AFY, APY, ALwt, ALonge, BMY, BFY, BPY, BLwt, BLonge,
ETMY, ETFY, ETPY, ETLwt, ETLonge, EPMY, EPFY, EPPY, EPLwt, EPLonge,
MY, FY, PY, Lwt, Longe, EBVM, EBVF, EBVP, EBVLWT, EBVLonge, Tmerit,
Year, Lac, Status from Yk29; quit;

proc SQL;  create table Yk49 as select distinct MMY, (CowID+1000153)
from Yk48; quit;

data ykn; set yk48; if Alonge=0 then k=.; run;

data Yk50; merge Yk49  Yk41 Yk47 Ykn YK33; run; quit;

proc sort data=Yk50; by k; run; quit;
proc surveyselect data=Yk50 Method=SEQ Samprate=57 out=Yk51;
strata k; run; quit;

data yk52; set Yk51; N1=uniform(1); run;
proc sort data=Yk52; by N1; run;
data Bull100 Cow100; set Yk52; if N1=<0.50 then output Bull100; else
output Cow100; run;

proc sql; create table cow101 as select distinct  _TEMA001, BullID,
CowID, Herd, Age, MMY,MFY,MPY,MLwt, MLonge, HMY, HFY, HPY, HLwt,
HLonge,
```

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AMY, AFY, APY, ALwt, ALonge, BMY, BFY, BPY, BLwt, BLonge, ETMY,
ETFY, ETPY, ETLwt, ETLonge, EPMY, EPFY, EPPY, EPLwt, EPLonge, MY,
FY, PY, Lwt, Longe, Year, Lac, Status, k from Cow100; quit;

data pro11;
set cow51 cow101; run;
proc sort data=Pro11; by _TEMA001; run; quit;

 filename out'C:\aireml\PY11.dat'; data sasuser.kkhan; set pro11;
file out; put  _Tema001 14. BullID 10. CowID 9. Herd 5. Age 4. MY
8.; run;
 filename out'C:\aireml\PY12.dat';data sasuser.kkhan; set pro11;
file out; put  _Tema001 14. BullID 10. CowID 9. Herd 5. Age 4. FY
7.; run;
 filename out'C:\aireml\PY13.dat';data sasuser.kkhan; set pro11;
file out; put  _Tema001 14. BullID 10. CowID 9. Herd 5. Age 4. PY
6.; run;
 filename out'C:\aireml\PY14.dat';data sasuser.kkhan; set pro11;
file out; put  _Tema001 14. BullID 10. CowID 9. Herd 5. Age 4. Lwt
6.; run;
 filename out'C:\aireml\PY15.dat';data sasuser.kkhan; set pro11;
file out; put  _Tema001 14. BullID 10. CowID 9. Herd 5. Age 4. Longe
7.; run;

Options noxwait xsync;
x C:\aireml\YP11.bat;  x C:\aireml\Y2M.bat; run;
      data one1; infile 'C:\AIREML\uni01.sln'; input _TEMa001 EBVM;
run; quit;
x C:\aireml\YP12.bat;  x C:\aireml\Y2M.bat; run;
      data two1; infile 'C:\AIREML\uni01.sln'; input _TEMa001 EBVF;
run; quit;
x C:\aireml\YP13.bat;  x C:\aireml\Y2M.bat; run;
      data three1; infile 'C:\AIREML\uni01.sln'; input _TEMa001
EBVP; run; quit;
x C:\aireml\YP14.bat;  x C:\aireml\Y2L.bat; run;
      data four1; infile 'C:\AIREML\uni01.sln'; input _TEMa001
EBVLwt; run; quit;
x C:\aireml\YP15.bat;  x C:\aireml\Y2lg.bat; run;
      data five1; infile 'C:\AIREML\uni01.sln'; input _TEMa001
EBVLonge; run; quit;

data Yk11KK; merge one1 two1 three1 four1 five1; by _TEMa001; run;
quit;

proc iml;
x= {0.32, 0, 0, 0, 0};/*economic values*/
use Yk11KK; read all var{EBVM EBVF EBVP EBVLWT EBVLonge} into k2;
k3=k2; k=k3*x; cname={TMerit};
create k1 from k [colname=cname]; append from k; quit;

data Yk53; merge Yk11KK k1; run; quit;
/*Bulls and dams*/
proc sql; create table Yk55 as
select distinct  _TEMA001, EBVM, EBVF, EBVP, EBVLWT, EBVLonge,
Tmerit
from Yk53
where  _TEMA001<1000000; quit;

/*F1 bulls*/
proc sql; create table Year1Bull as
```

```
select distinct  _TEMA001, EBVM, EBVF, EBVP, EBVLWT, EBVLonge,
TMerit
from Yk55
where  _TEMA001>=70153; quit;

proc sort data= pro11; by _TEMA001; run;
data Ykk57; merge Yk53 Pro11; by _TEMA001; run; quit;

proc sql; create table BullF1 as select distinct SireID, DamID, BMY,
BFY, BPY, BLwt, BLonge from YK5; quit;
data BullF; merge Year1Bull BullF1; run;
proc sql; create table YKK56 as select distinct _Tema001, (_Tema001)
as BulID, SireID, DamID, BMY, BFY, BPY, BLwt, BLonge, Tmerit from
BullF; quit;
proc sql; create table YKKK56a as select distinct BulID, SireID,
DamID, BMY, BFY, BPY, BLwt, Blonge, TMerit from YKK56; quit;

data xBull1; set YKKK56a Bull51F; run;

proc sql; create table Ykk58 as select distinct
 _TEMA001, BullID, CowID, Herd, Age, MMY,MFY,MPY,MLwt, MLonge, HMY,
HFY, HPY, HLwt, HLonge,
 AMY, AFY, APY, ALwt, ALonge, BMY, BFY, BPY, BLwt, BLonge, ETMY,
ETFY, ETPY, ETLwt, ETLonge,
 EPMY, EPFY, EPPY, EPLwt, EPLonge, MY, FY, PY, Lwt, Longe, EBVM,
EBVF, EBVP, EBVLWT, EBVLonge,
 Tmerit, Year, k from Ykk57 where MY>.; quit;

data ghf; set YKk58; if alonge=0 then Lac=1; if alonge=0 then
Status=2; if alonge=0 then Age=4; run;

proc sql; create table Yk59 as select distinct  _TEMA001,(_TEMA001)
as CID, BullID,(BullID) as SireID, CowID, (CowID) as DamID, Herd,
Age, MMY,MFY,MPY,MLwt, MLonge, HMY, HFY, HPY, HLwt, HLonge, AMY,
AFY, APY, ALwt, ALonge, BMY, BFY, BPY, BLwt, BLonge, ETMY, ETFY,
ETPY, ETLwt, ETLonge,EPMY, EPFY, EPPY, EPLwt, EPLonge, MY, FY, PY,
Lwt, Longe, EBVM, EBVF, EBVP, EBVLWT, EBVLonge, Tmerit, Year, Lac,
Status, k from ghf; quit;

proc sql; create table Year1Pro as select distinct
 (CID) as CowId, SireID, DamID, Herd, Age, MMY,MFY,MPY,MLwt, MLonge,
HMY, HFY, HPY, HLwt, HLonge,AMY, AFY, APY, ALwt, ALonge, BMY, BFY,
BPY, BLwt, BLonge, ETMY, ETFY, ETPY, ETLwt, ETLonge, EPMY, EPFY,
EPPY, EPLwt, EPLonge, MY, FY, PY, Lwt, Longe, EBVM, EBVF, EBVP,
EBVLWT, EBVLonge, Tmerit, Year, Lac, Status, k from Yk59; quit;

proc surveyselect data=Top90 Method=SRS Samprate=95 out=Yk67; strata
k; run; quit;
data yk68; set Yk67 (OBS=8900); run; quit;

Proc iml;
n=8900;
sigma8= {   34453.13     754.64      539.33      205.75      2552.92,
              754.64      38.92       29.63       40.24        89.85,
              539.33      29.63       37.09       39.64        51.05,
              205.75      40.24       39.64       88.76        15.72,
             2552.92      89.85       51.05       15.72      5548.20};
                                  /*Temporary environmental
effects*/
          mu8={0, 0, 0, 0, 0};
```

```
cname={ETMY ETFY ETPY ETLwt ETLonge}; g8 =(root(sigma8)); /* Upper
Triangular Cholesky decomposition of Cov matrix */
z8=normal(repeat(mu8`, n, 1)); y8= z8*g8;
create empdist8 from y8 [colname=cname]; append from y8; quit;

Proc IML;
use empdist8; read all var {ETMY ETFY ETPY ETLwt ETLonge}into Yk69;
use Yk68; read all var {ETMY ETFY ETPY ETLwt ETLonge} into Yk70;
Yk71=Yk69-Yk70; use Yk68; read all var {MY FY PY Lwt Longe} into
Yk72; Yk73=Yk70+Yk72; HLL={MY FY PY Lwt Longe};
create Yk74 from Yk73 [colname=HLL]; append from Yk73; quit;

proc iml; use Yk68; read all var {Age Year Lac} into Yk75;
Yk76=Yk75+1;
colna={Age Year Lac}; create Yk77 from Yk76 [colname=colna]; append
from Yk76; quit;

proc sql; create table Yk78 as select distinct COWID, SireID, DamID,
Herd, MMY, MFY, MPY, MLWT, MLonge, HMY, HFY, HPY, HLwt, Hlonge, AMY,
AFY, APY, Alwt, Alonge, BMY, BFY, BPY, BLwt, BLonge, EPMY, EPFY,
EPPY, EPLwt, EPLonge, Status,k from Yk68; quit;

data Yk79; merge Yk78 empdist8 Yk74 Yk77; run; quit;

proc sql;
create table Year2 as
select distinct COWID, SireID, DamID, Herd, MMY, MFY, MPY, MLWT,
MLonge, HMY, HFY, HPY, HLwt, Hlonge,AMY, AFY, APY, Alwt, Alonge,
BMY, BFY, BPY, BLwt, BLonge, EPMY, EPFY, EPPY, EPLwt, EPLonge, ETMY,
ETFY, ETPY, ETLwt, ETLonge, MY, FY, PY, LWT, Longe, age, Year, Lac,
status, k from Yk79 where Age<11; quit;
```

APPENDIX THREE (B)

Average economic merit (US$) with standard deviation (bar) for fat, protein, liveweight and longevity under progeny and parent average breeding schemes with three different selection objectives

Figure B 7.7: Average economic merit (US$) with standard deviation (bar) for different traits under parent average testing (PAT) and progeny testing (PT) breeding schemes with a selection objective of milk merit for all cows born in a particular year

Figure 7.7.1. Average economic merit (US$) for fat yield

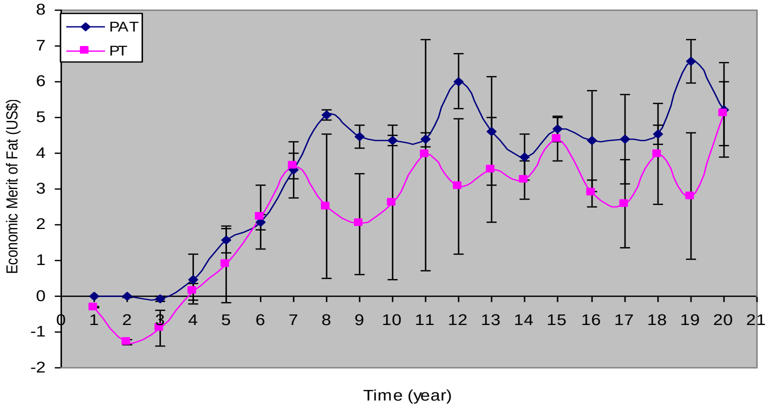

Figure 7.7.2. Average economic merit (US$) for protein yield

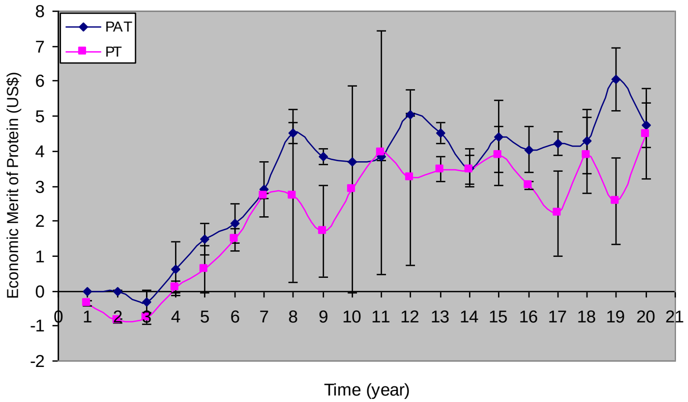

Figure 7.7.3. Average economic merit (US$) for liveweight

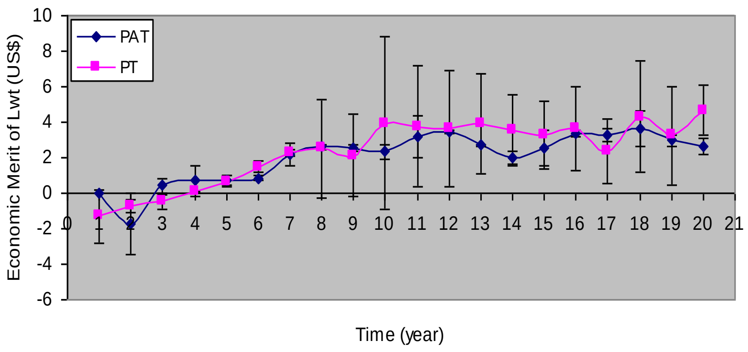

Figure 7.7.4. Average economic merit (US$) for longevity

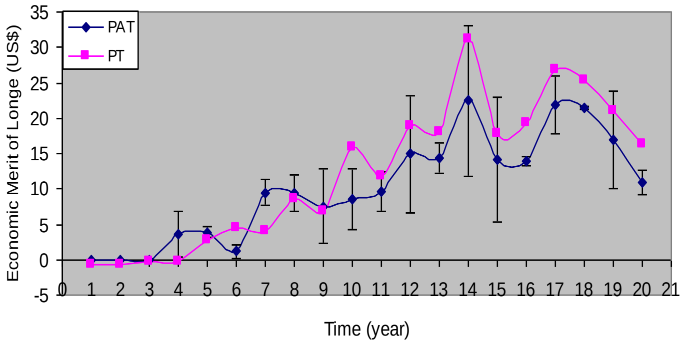

Figure B 7.8: Average economic merit (US$) with standard deviation (bar) for different traits under parent average testing (PAT) and progeny testing (PT) breeding schemes with selection objective of milk and survival merit for all cows born in a particular year

Figure 7.8.1. Average economic merit (US$) for fat yield

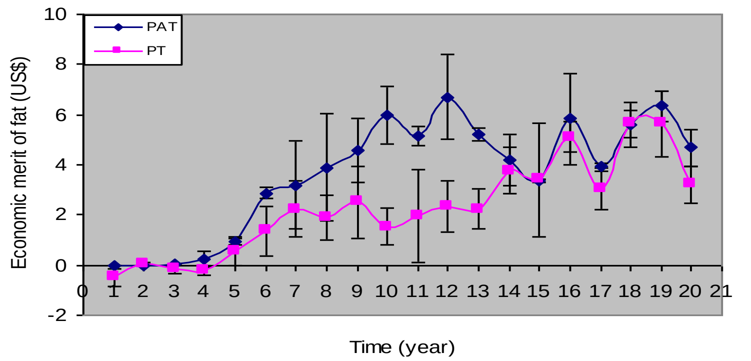

Figure 7.8.2. Average economic merit (US$) for protein yield

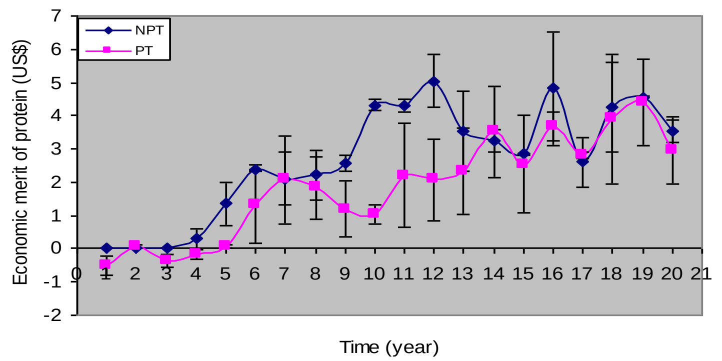

Figure 7.8.3. Average economic merit (US$) for live w eight

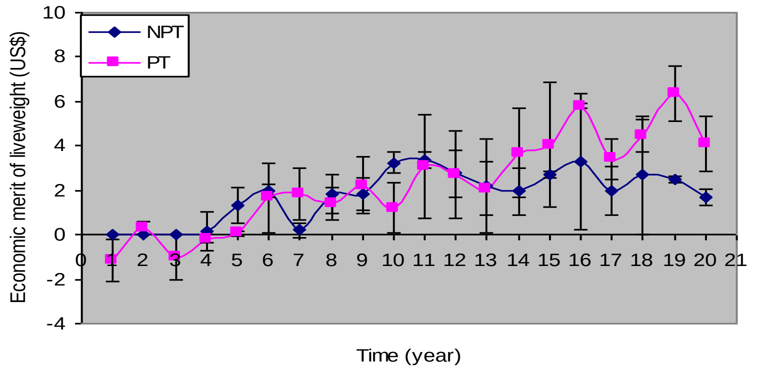

Figure 7.8. 4. Average economic merit (US$) for Longevity

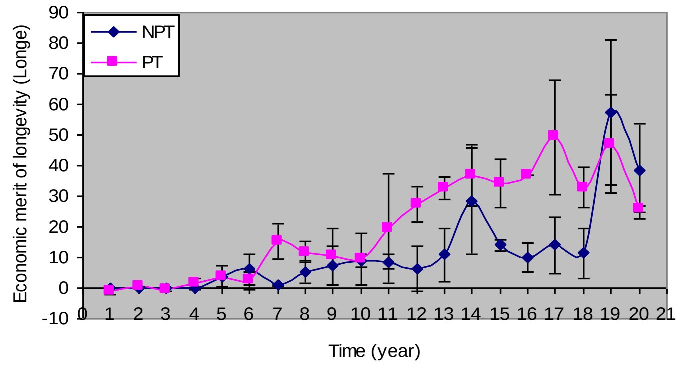

Figure B 7.9: Average economic merit (US$) with standard deviation (bar) for different traits under parent average testing (PAT) and progeny testing (PT) breeding schemes with a selection objective of total merit for all cows born in a particular year

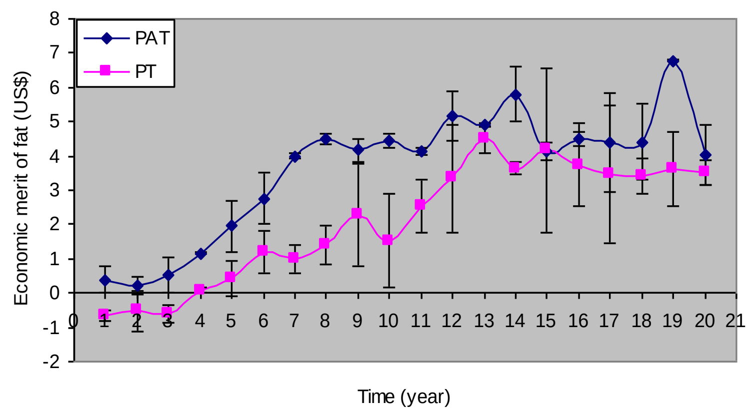

Figure 7.9.1. Average economic merit US$) for fat yield

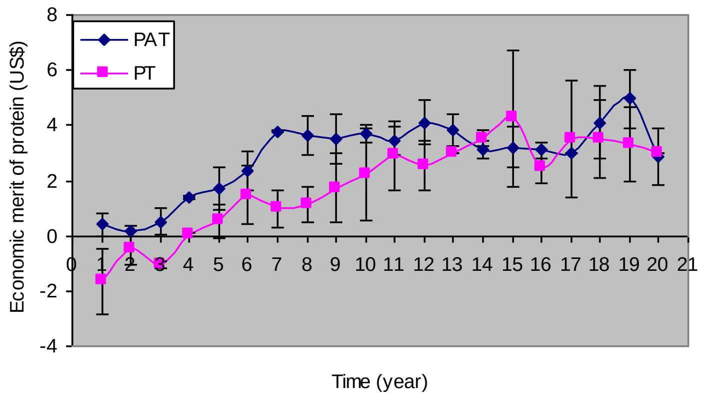

Figure 7.9.2. Average economic merit (US$) for protein yield

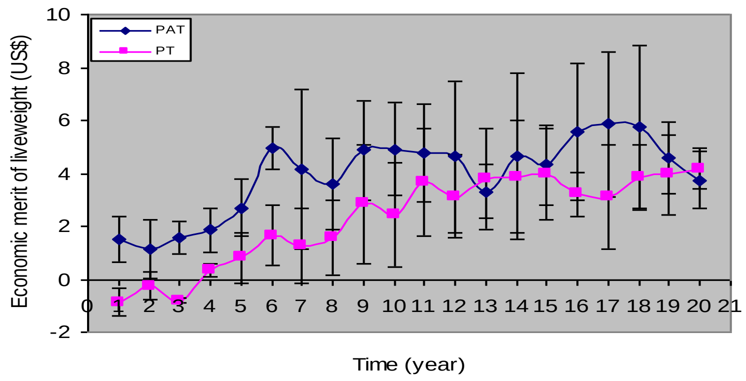

Figure 7.9.3. Average economic merit (US$) for live w eight

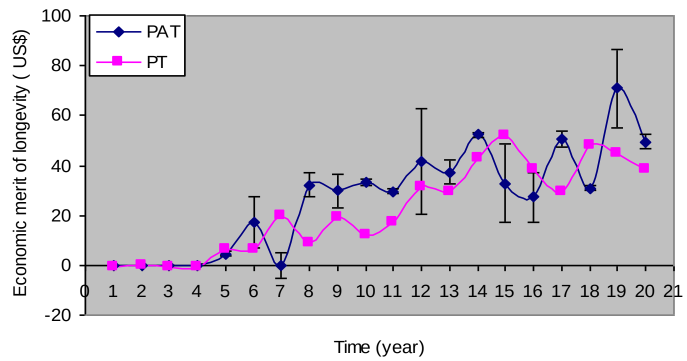

Figure 7.9.4. Average economic merit (US$) for longevity

Figure B 7.10: Average economic merit (US$) with standard deviation (bar) for different traits under parent average testing and progeny testing (PT) breeding schemes with a selection objective of milk merit for selected bulls born in a particular year

Figure 7.10.1. Average economic merit (US$) for fat yield

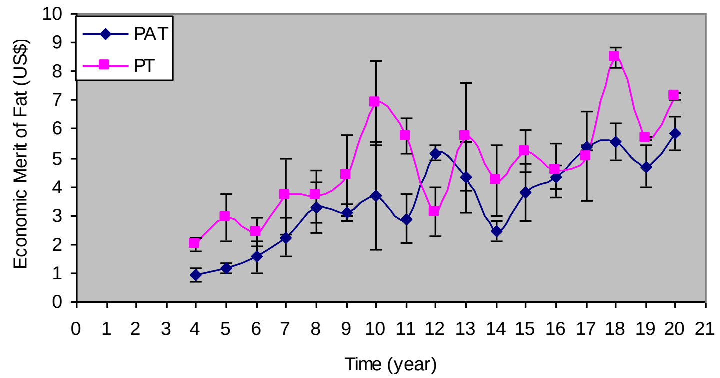

Figure 7.10.2. Average economic merit (US$) for protein yield

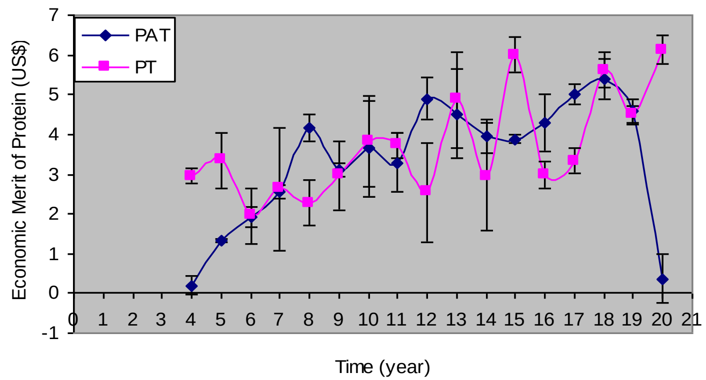

Figure 7.10. 3. Average economic merit (US$) for livew eight

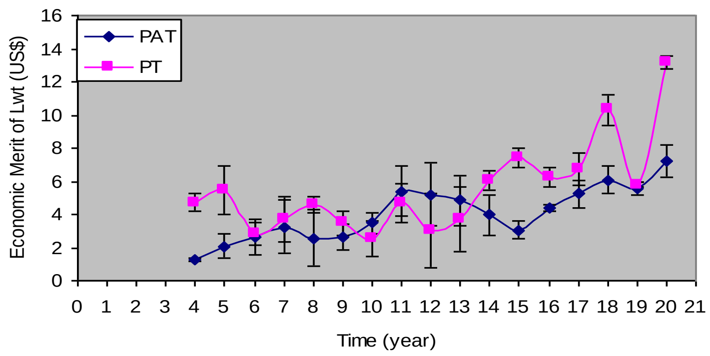

Figure 7.10.4. Average economic merit (US$) for longevity

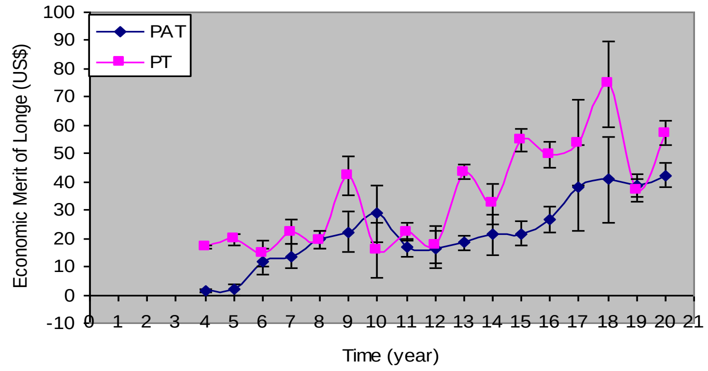

Figure B 7.11: Average economic merit (US$) with standard deviation (bar) for different traits under parent average testing and progeny testing (PT) breeding schemes with a selection objective of milk and survival merit for selected bulls born in a particular year

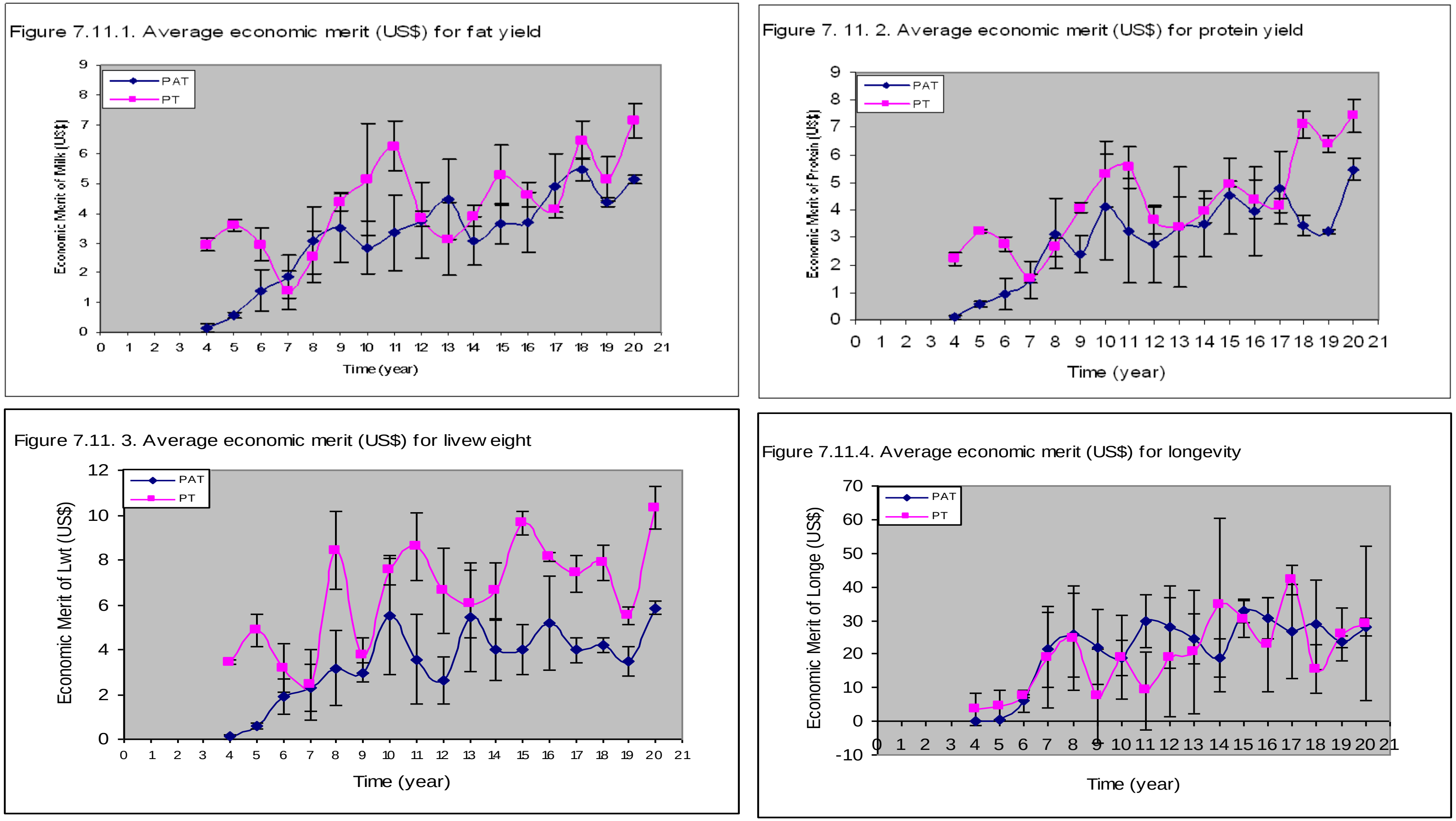

Figure B 7.12: Average economic merit (US$) with standard deviation (bar) for different traits under parent average testing (PAT) and progeny testing (PT) breeding schemes with a selection objective of total merit for selected bulls born in a particular year